

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 8, 2001, 08:52:56 ; Search time 21.65 seconds
(without alignments) 268.888 million cell updates/sec

Title: US-09-497-591-1
Perfect score: 200
Sequence: 1 ANSFLXXLRHSLRXRCIXX.....XXAKXIFQNVDTLAFWSKH 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP archaea: *
2: SP bacteria: *
3: SP fungi: *
4: SP human: *
5: SP invertebrate: *
6: SP mammal: *
7: SP mhc: *
8: SP organelle: *
9: SP phage: *
10: SP plant: *
11: SP rodent: *
12: SP unclassified: *
13: SP vertebrate: *
14: SP virus: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	158	79.0	456	6 Q9TTR0	Q9TTR0 canis faml
2	130	75.0	459	6 Q9GLP2	Q9GLP2 sus scrofa
3	105	52.5	482	11 Q63207	Q63207 ratus norv
4	93	46.5	444	4 Q14339	Q14339 homo sapien
5	91	45.5	481	11 Q54740	Q54740 mus musculu
6	91	45.5	481	11 Q88947	Q88947 mus musculu
7	89	44.5	218	4 Q14668	Q14668 homo sapien
8	85	42.5	469	6 Q9GMD9	Q9GMD9 ornithorhyn
9	82	41.0	650	4 Q16519	Q16519 homo sapien
10	82	41.0	650	4 Q9NSD0	Q9NSD0 homo sapien
11	80	40.0	100	4 Q15253	Q15253 homo sapien
12	80	40.0	446	11 Q61109	Q61109 mus musculu
13	79	39.5	138	6 Q28994	Q28994 sus scrofa
14	77	38.5	456	4 Q14316	Q14316 homo sapien
15	75	37.5	648	6 Q29094	Q29094 sus scrofa
16	74	37.0	607	13 Q91001	Q91001 gallus gall
17	68	34.0	608	13 Q9PTW7	Q9PTW7 struthio ca
18	65.5	32.8	422	4 Q15213	Q15213 homo sapien
19	64	32.0	25	11 Q9QVH6	Q9QVH6 ratus sp.

20	63	31.5	98	13 P82807	P82807 notechis sc
21	62	31.0	673	11 Q61592	Q61592 mus musculu
22	61	30.5	674	11 Q63772	Q63772 ratus norv
23	60	30.0	678	4 Q14393	Q14393 homo sapien
24	56	28.0	202	4 Q14669	Q14669 homo sapien
25	52	26.0	724	4 Q9H6S7	Q9H6S7 homo sapien
26	51.5	25.8	594	10 Q9S1G9	Q9S1G9 arabisdops
27	51	25.5	16	4 Q9UC55	Q9UC55 homo sapien
28	50.5	25.2	459	10 Q9SE22	Q9SE22 oryza sativ
29	50	25.0	615	10 Q9LU67	Q9LU67 arabisdops
30	49.5	24.8	510	2 Q9POS4	Q9POS4 ureaplasma
31	49.5	24.8	603	10 Q9LPG7	Q9LPG7 arabisdops
32	49.5	24.8	608	10 Q9XFP6	Q9XFP6 medicago sa
33	48.5	24.2	196	10 Q04284	Q04284 selaginella
34	48.5	24.2	593	10 Q9LUD3	Q9LUD3 arabisdops
35	48.5	24.2	2454	3 Q9UVP2	Q9UVP2 emericella
36	48.5	24.2	2454	3 Q9UV56	Q9UV56 emericella
37	48	24.0	606	3 Q9US07	Q9US07 schizosacch
38	47.5	23.8	506	10 Q9SPR0	Q9SPR0 oryza sativ
39	47.5	23.8	506	10 Q9SE23	Q9SE23 oryza sativ
40	47.5	23.8	543	10 Q9MB23	Q9MB23 arabisdops
41	47.5	23.8	589	10 Q9LMS2	Q9LMS2 arabisdops
42	47	23.5	221	6 Q9N111	Q9N111 ovis aries
43	47	23.5	390	4 Q9UG06	Q9UG06 homo sapien
44	47	23.5	538	4 Q9YAC9	Q9YAC9 homo sapien
45	47	23.5	574	4 Q9H1G5	Q9H1G5 homo sapien

ALIGNMENTS

RESULT 1					
Q9TTR0	1	PRELIMINARY:	PRT:	456 AA.	
AC Q9TTR0:					
DT 01-MAY-2000 (TREMBLrel. 13, Created)					
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)					
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)					
DE PROTEIN C PRECURSOR.					
GN PROC.					
OS Canis familiaris (Dog).					
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.					
OC NCBI_TaxID=9615;					
RN [1]					
RP SEQUENCE FROM N.A.					
RA Leeb T., Kopp T., Deppe A., Breen M., Matls U., Brunberg L.,					
RA Breenig B.;					
RT "Molecular characterization and chromosomal assignment of the canine					
RT protein C gene".					
RL Mamm. Genome 10:135-139(1999).					
RN [2]					
RP SEQUENCE FROM N.A.					
RX MEDLINE=99371952; PubMed=10443005;					
RA Leeb T., Pfeiffer I., Kopp T., Deppe A., Breenig B.;					
RT "Analysis of canine protein C gene polymorphisms".					
RL Anim. Genet. 30:237-238(1999).					
CC -1- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.					
CC -1- SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).					
DR EMBL; AJ001979; CAA05126.1; -					
DR HSSP; P04070; IPCU.					
DR InterPro; IPR000152; -					
DR InterPro; IPR000561; -					
DR InterPro; IPR001254; -					
DR InterPro; IPR001314; -					
DR InterPro; IPR001881; -					
DR InterPro; IPR002383; -					
DR Pfam; PF00008; EGF. 2.					
DR Pfam; PF00089; trypsin. 1.					
DR Pfam; PF00594; gla. 1.					
DR PRINTS; PR00722; CHYMOTRYPSIN.					
DR PRINTS; PR00001; GLABLOOD.					

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DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR SMART: SM00181; EGF; 1.
KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease; Signal.
FT SIGNAL; 1
FT CHAIN; 43 192
FT CHAIN; 193 194
FT CHAIN; 195 456
FT CHAIN; PROTEIN C CONNECTING DIPEPTIDE.
FT CHAIN; PROTEIN C HEAVY CHAIN.
SO SEQUENCE 456 AA; 50813 MW; 7AD3A8C1C34E59FE CRC64;

Query Match 79.0%; Score 158; DB 6; Length 456;
Best Local Similarity 68.2%; Pred. No. 5.7e-19;
Matches 30; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSLKRCIXXCDFXAKXIFQNDPDLAFMSKH 44
DB 43 ANSFLERIRAGSLERECMEETCFEERAKEIFQNDPDLAFMSKY 86

RESULT 2
Q9GLP2 PRELIMINARY; PRT; 459 AA.
AC Q9GLP2;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-NOV-1996 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE PROTEIN C.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP TISSUE=LIVER;
RA Grimm D.R., Colter M.B., Kim H.;
RT Cloning of the complete cDNA sequences encoding porcine factor V and
RL protein C.;
RL EMBL: AF191307; AAC28380.1; -
DR EMBL: AF191307; AAC28380.1; -
SO SEQUENCE 459 AA; 51866 MW; 8541AAC14CC16D09 CRC64;

Query Match 65.0%; Score 130; DB 6; Length 459;
Best Local Similarity 56.8%; Pred. No. 4e-14;
Matches 25; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSLKRCIXXCDFXAKXIFQNDPDLAFMSKH 44
DB 42 ANSFLERIRAGSLERECMEETCFEERAKEIFQNDPDLAFMSKY 85

RESULT 3
Q63207 PRELIMINARY; PRT; 482 AA.
AC Q63207;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE FACTOR X.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;

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RX MEDLINE=96093366; PubMed=8578539;
RA Stanton C., Ross R.P., Hutson S.;
RT "Evidence for competition between vitamin K-dependent clotting factors
RT for intracellular processing by the vitamin K-dependent gamma-
RT carboxylase.";
RL Thromb. Res. 80:63-73(1995).
CC -1- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.
CC -1- SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).
DR EMBL: X79807; CAA56202.1; -
DR HSSP: P00742; 1XKA.
DR MEROPS; S01.216; -.
DR Interpro: IPR000152; -.
DR Interpro: IPR000294; -.
DR Interpro: IPR000561; -.
DR Interpro: IPR000742; -.
DR Interpro: IPR001254; -.
DR Interpro: IPR001314; -.
DR Interpro: IPR001314; -.
DR Interpro: IPR001881; -.
DR Interpro: IPR002383; -.
DR Pfam: PF00008; EGF; 2.
DR Pfam: PF00089; trypsin; 1.
DR Pfam: PF00594; gla; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR SMART: SM00020; TRYP_SPC; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease.
SO SEQUENCE 482 AA; 54265 MW; 0284678E3954A698 CRC64;

Query Match 52.5%; Score 105; DB 11; Length 482;
Best Local Similarity 38.6%; Pred. No. 8.9e-10;
Matches 17; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSLKRCIXXCDFXAKXIFQNDPDLAFMSKH 44
DB 41 ANSFEETKGNLERECVEETCFEERAEVDEDKTTFMNKY 84

RESULT 4
Q14339 PRELIMINARY; PRT; 444 AA.
AC Q14339;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE PREPROFACTOR VIIb PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=86205965; PubMed=3486420;
RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,
RA Woodbury R.G., Hart C.E., Insley M., Kistiel W., Kurachi K.,
RA Davie E.W.;
RT "Characterization of a cDNA coding for human factor VII.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
CC -1- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.
CC -1- SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).
DR EMBL: M13232; AAA88041.1; -
DR HSSP: P08709; 1BF9.
DR Interpro: IPR000152; -.
DR Interpro: IPR000294; -.

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DR InterPro: IPR000561; -
DR InterPro: IPR000742; -
DR InterPro: IPR001254; -
DR InterPro: IPR001314; -
DR InterPro: IPR001881; -
DR InterPro: IPR002383; -
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00089; trypsin; 1.
DR Pfam: PF00594; gla; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
DR SMART: SM00020; Tryp-spec; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease; Signal.
FT SIGNAL 1 38 POTENTIAL.
FT SIGNAL 1 60 POTENTIAL.
FT CHAIN 39 190 COAGULATION FACTOR VII.
FT CHAIN 191 444 COAGULATION FACTOR VII.
SQ SEQUENCE 444 AA; 49320 MW; 2E74EAFD2FADEF2A4 CRC64;

Query Match 46.5%; Score 93; DB 4; Length 444;
Best Local Similarity 46.3%; Pred. No. 9.6e-08;
Matches 19; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

Oy - 1 ANSFLXLRHGSILXRXCIXICDFFXXAKXIFQNVDTLAFW 41
DB 39 ANAFLEELRPGSLERECKEBCGCFEAREITFDAERTKLFW 79

RESULT 5
054740 PRELIMINARY; PRT: 481 AA.
AC 054740;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE COAGULATION FACTOR X PRECURSOR (EC 3.4.21.6).
GN FA10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP TISSUE: LIVER;
RC SEQUENCE FROM N.A.
RA Heldmann H.H., Kontermann R.E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO SERINE PROTEASES, TRYPsin FAMILY.
CC -1- SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).
DR EMBL: AJ222677; CAA10933.1; -
DR HSSP: P00742; 1XKB.
DR MGD: S01.216; -
DR InterPro: IPR000152; -
DR InterPro: IPR000294; -
DR InterPro: IPR000561; -
DR InterPro: IPR000742; -
DR InterPro: IPR001254; -
DR InterPro: IPR001881; -
DR InterPro: IPR002383; -
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00089; trypsin; 1.
DR Pfam: PF00594; gla; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.

DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
DR SMART: SM00001; EGF-like; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease; Signal.
FT SIGNAL 1 40 POTENTIAL.
FT CHAIN 41 481 COAGULATION FACTOR X.
SQ SEQUENCE 481 AA; 53985 MW; CF702D5E5FE97AE CRC64;

Query Match 45.5%; Score 91; DB 11; Length 481;
Best Local Similarity 34.1%; Pred. No. 2.3e-07;
Matches 15; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

Oy 1 ANSFLXLRHGSILXRXCIXICDFFXXAKXIFQNVDTLAFWSKH 44
DB 41 ANSFEEFRKGNLERECMEICSYEVREITFEDKTEYWTYK 84

RESULT 6
088947 PRELIMINARY; PRT: 481 AA.
AC 088947;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE COAGULATION FACTOR X PRECURSOR.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP TISSUE: LIVER;
RC STRAIN=C57BL6 X CBA; TISSUE=LIVER;
RX MEDLINE=96347933; PubMed=9684791;
RA Liang Z., Cooper A., Deford M.E., Carmeliet P., Collen D.,
RA Castellino F.J., Rosen E.D.;
RT "Cloning and characterization of a cDNA encoding murine coagulation factor X";
RL Thromb. Haemost. 80:87-91(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129Sj;
RA Cooper A., Liang Z., Castellino F.J., Rosen E.D.;
RT "Cloning and Characterization of the Murine Factor X Gene";
RL Thromb. Haemost. 0:0-0(2000).
CC -1- SIMILARITY: TO SERINE PROTEASES, TRYPsin FAMILY.
CC -1- SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).
DR EMBL: AF087644; AAC36345.1; -
DR EMBL: AF211347; AAF22980.1; -
DR HSSP: P00742; 1XKA.
DR MGD: MGI.103107; F10.
DR InterPro: IPR000152; -
DR InterPro: IPR000294; -
DR InterPro: IPR000561; -
DR InterPro: IPR000742; -
DR InterPro: IPR001254; -
DR InterPro: IPR001881; -
DR InterPro: IPR002383; -
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00089; trypsin; 1.
DR Pfam: PF00594; gla; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.

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DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
DR SMART; SM00020; TRYP-SPEC; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KM Serine protease; Signal.
FT SIGNAL 1 40 POTENTIAL.
FT CHAIN 41 481 COAGULATION FACTOR X.
SQ SEQUENCE 481 AA; 54018 MW; 8AC09D5E9FD271E CRC64;

Query Match
Best Local Similarity 45.5%; Score 91; DB 11; Length 481;
Matches 15; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANSFLXLRHGSILKRCIXIXICDFXAKXIFQNVDTLAFWSKH 44
    ||| : : : : : : : : : : : : : : : : : : :
Db 41 ANSFEEFKKGNLERECMEICSYEEVREIFEDDEKTRKYWKY 84

RESULT 7
ID 014668 PRELIMINARY; PRT; 218 AA.
AC 014668;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-NOV-1996 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PROLINE-RICH GLA PROTEIN 1.
GN PRGPI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1997).
DR EMBL; AF009242; AAB67070.1; -.
DR HSSP; P00740; ICFH.
DR InterPro; IPR000294; -.
DR InterPro; IPR002383; -.
DR Pfam; PF00594; glA; 1.
DR PRINTS; PR00001; GLABLOOD.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR SMART; SM00069; GLA; 1.
SQ SEQUENCE 218 AA; 24947 MW; 26538A61AB0AEB98 CRC64;

Query Match
Best Local Similarity 44.5%; Score 89; DB 4; Length 218;
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANSFLXLRHGSILKRCIXIXICDFXAKXIFQNVDTLAFWSKH 44
    ||| : : : : : : : : : : : : : : : : : : :
Db 21 ANGFEEIRQGNIERECKEPCFEAREAFENNEKTRKRWSTY 64

RESULT 8
ID 09GMD9 PRELIMINARY; PRT; 469 AA.
AC 09GMD9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE COAGULATION FACTOR X.
OS Ornithorhynchus anatinus (Duckbill platypus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
OX NCBI_TaxID=9258;
RN [1]
RP SEQUENCE FROM N.A.
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RA Pourafshar M.M., Hellman L.L.;
RT "Identification and structural analysis of three serine proteases in a
RT monotreme, platypus, Ornithorhynchus anatinus.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF275654; AAC00453.1; -.
SQ SEQUENCE 469 AA; 52196 MW; 4C6C230D0758F6A CRC64;

Query Match
Best Local Similarity 42.5%; Score 85; DB 6; Length 469;
Matches 15; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANSFLXLRHGSILKRCIXIXICDFXAKXIFQNVDTLAFWS 42
    ||| : : : : : : : : : : : : : : : : : : :
Db 41 ANSFLFEELKGNLERECNEETCSYEAREVEFDTRKNEFMN 82

RESULT 9
ID 016519 PRELIMINARY; PRT; 650 AA.
AC 016519;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PROTEIN S PRECURSOR.
GN PROS1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=6633649; PubMed=2944113;
RA Lundwall A., Deckowski W., Cohen E., Shaffer M., Mahr A., Dahlback B.,
RA Stenflo J., Wydro R.;
RT "Isolation and sequence of the cDNA for human protein S, a regulator
RT of blood coagulation.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:6716-6720(1986).
DR EMBL; M1438; AAA60181.1; -.
DR HSSP; P07204; IEGT.
DR InterPro; IPR000152; -.
DR InterPro; IPR000294; -.
DR InterPro; IPR000561; -.
DR InterPro; IPR001791; -.
DR InterPro; IPR001881; -.
DR InterPro; IPR002383; -.
DR Pfam; PF00008; EGF; 4.
DR Pfam; PF00054; laminin_G; 1.
DR PRINTS; PR00001; GLABLOOD.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01187; EGF_CA; 2.
DR SMART; SM00282; Lang; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat;
KM Signal.
FT SIGNAL 1 15 POTENTIAL.
FT CHAIN 16 650 POTENTIAL.
SQ SEQUENCE 650 AA; 72462 MW; 9A8C044C503BF474 CRC64;

Query Match
Best Local Similarity 41.0%; Score 82; DB 4; Length 650;
Matches 16; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANSFLXLRHGSILKRCIXIXICDFXAKXIFQNVDTLAFWSKH 44
    ||| : : : : : : : : : : : : : : : : : : :
Db 16 ANSFLFEELKGNLERECIEICNKEAREVEFNDPDEYFYPKY 59

RESULT 10
```

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Q9NSDO
ID Q9NSDO PRELIMINARY; PRT; 650 AA.
AC Q9NSDO:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE PROTEIN S PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER.
RA Wydro R., Cohen E., Dackowski W., Stenflo J., Lundwall A.,
RA Dahlback B.,
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; X12892; CAA31383.1; -.
DR InterPro: IPR000152; -.
DR InterPro: IPR000294; -.
DR InterPro: IPR000561; -.
DR InterPro: IPR001791; -.
DR InterPro: IPR001881; -.
DR InterPro: IPR002383; -.
DR Pfam: PF00008; EGF_4.
DR Pfam: PF00054; laminin_G; 1.
DR Pfam: PF00594; gla; 1.
DR PRINTS: PR00001; GLABLOOD.
DR PROSITE: PS00010; ASX_HYDROXYL; 3.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 3.
DR PROSITE: PS01187; EGF_CA; 2.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR SMART: SM00179; EGF_CA; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat;
KW Signal.
FT SIGNAL 1 15 POTENTIAL.
FT CHAIN 16 650 POTENTIAL.
SQ SEQUENCE 650 AA; 72480 MW; C67345EC8645174 CRC64;

Query Match 41.0%; Score 82; DB 4; Length 650;
Best Local Similarity 36.4%; Pred. No. 1.2e-05;
Matches 16; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

OY 1 ANSFLXLRHGSIXKXCIXXICDFFXAKXIFQNVDDTLAFMSKH 44
DB 16 ANSLLETKQGNLRECEIEELCNKEAREVFNDETDYFYPKY 59

RESULT 11
O15253 PRELIMINARY; PRT; 100 AA.
AC Q15253:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE THROMBIN PRECURSOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RL MEDLINE=87182874; PubMed=3471151;
RA MacGillivray R.T., Irwin D.M., Gulino E.R., Stone J.C.;
RT "Recombinant genetic approaches to functional mapping of thrombin.";
RL Ann. N.Y. Acad. Sci. 485:73-79(1986).
DR EMBL: M31031; AAA60220.1; -.
DR HSSP: P00735; 2PFI.
DR InterPro: IPR000294; -.
DR InterPro: IPR002383; -.

DR Pfam: PF00594; gla; 1.
DR PRINTS: PR00001; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS00025; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR SMART: SM00020; TRYP_SPC; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolyase; Repeat;
KW Serine protease.
SQ SEQUENCE 446 AA; 50318 MW; 482FD09BEFDA6870 CRC64;
```

```
DR Pfam: PF00594; gla; 1.
DR PRINTS: PR00001; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR SMART: SM00059; GLA; 1.
FT SIGNAL 1 43 POTENTIAL.
FT CHAIN 44 >100 POTENTIAL.
FT NON_TER 100 100
SQ SEQUENCE 100 AA; 11302 MW; FD0E5D0174E1F6FE CRC64;
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```
Query Match 40.0%; Score 80; DB 4; Length 100;
Best Local Similarity 34.1%; Pred. No. 3.5e-06;
Matches 15; Conservative 9; Mismatches 20; Indels 0; Gaps 0;
```

```
OY 1 ANSFLXLRHGSIXKXCIXXICDFFXAKXIFQNVDDTLAFMSKH 44
DB 44 ANTFLEVRKGNLRECEVETCSYEAFEALESSTATVFMARY 87
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RESULT 12

O61109 PRELIMINARY; PRT; 446 AA.

```
AC O61109:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE COAGULATION FACTOR VII.
GN CF7 OR FVII.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER.
RX MEDLINE=96276538; PubMed=8701412;
RA Idusogie E., Rosen E., Geng J.P., Carmeliet P., Collen D.,
RA Castellino F.;
RT "Characterization of a cDNA encoding murine coagulation factor VII.";
RL Thromb. Haemost. 75:481-487(1996).
CC -1 SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.
CC -1 SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).
DR EMBL: U44795; AAC52570.1; -.
DR HSSP: P08709; 1BP9.
DR MGD: MGI:109325; F7.
DR InterPro: IPR000152; -.
DR InterPro: IPR000294; -.
DR InterPro: IPR000561; -.
DR InterPro: IPR001064; -.
DR InterPro: IPR001254; -.
DR InterPro: IPR001314; -.
DR InterPro: IPR001881; -.
DR InterPro: IPR002086; -.
DR InterPro: IPR002383; -.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00089; trypsin; 1.
DR Pfam: PF00594; gla; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR PROSITE: PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR SMART: SM00020; TRYP_SPC; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolyase; Repeat;
KW Serine protease.
SQ SEQUENCE 446 AA; 50318 MW; 482FD09BEFDA6870 CRC64;
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Query Match 40.0%; Score 80; DB 11; Length 446;
Best Local Similarity 43.9%; Pred. No. 1.7e-05;
Matches 18; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANSLXLRHGSLSKRCIXXICDPXAKXIFQNVDDTLAFW 41
DB 42 ANSLLELWPGSLERECNCSFEARREIFKSPERTKQFW 82

RESULT 13

Q28994 PRELIMINARY; PRT; 138 AA.

AC Q28994;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE MATURIN PORCINE FACTOR IX (FRAGMENT).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=96003866; PubMed=7568220;
RA Brandstetter H., Bauer M., Huber R., Lollier P., Bode W.;
RT "X-ray structure of clotting factor IXa: active site and module
structure related to Xase activity and hemophilia B.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:9796-9800(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Lollier P.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U51135; AAA96318.1; -.
DR HSP: P00740; 11XA.
DR InterPro: IPR000152; -.
DR InterPro: IPR000294; -.
DR InterPro: IPR000561; -.
DR InterPro: IPR000742; -.
DR InterPro: IPR001438; -.
DR InterPro: IPR001881; -.
DR Pfam: PF0002383; -.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; g1a; 1.
DR PRINTS: PR00010; EGFBL00D.
DR PRINTS: PR00001; GLABLO0D.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR SMART: SM00001; EGF-like; 1.
KM Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
FT NON_TER 1 138
FT NON_TER 1 138
SQ SEQUENCE 138 AA; 15515 MW; 793BABDE4D5FAFAD CRC64;

Query Match 39.5%; Score 79; DB 6; Length 138;
Best Local Similarity 38.2%; Pred. No. 7.3e-06;
Matches 13; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 11 GSLKRCIXXICDPXAKXIFQNVDDTLAFWSKH 44
DB 4 GNLRECEMEKCSFEAREVENTERTTEFWKQY 37

RESULT 14

ID Q14316 PRELIMINARY; PRT; 456 AA.
AC Q14316;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1999 (TREMBLrel. 11, Last sequence update)

DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE F9 (COAGULATION FACTOR IX (PLASMA THROMBOPLASTIC COMPONENT, CHRISTMAS
DISEASE, HAEMOPHILIA B)) (FACTOR IX).
GN F9 OR FACTOR IX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bird C.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 3-19 FROM N.A.
RX MEDLINE=88327116; PubMed=3416069;
RA Reitsma P.A., Bertina R.M., Ploos van Amstel J.K., Riemens A.,
Riet E.;
RT "The putative factor IX gene promoter in hemophilia B Leyden.";
RL Blood 72:1074-1076(1988).
CC -1- SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY.
CC -1- SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).
DR EMBL: AL033403; CAA21954.1; -.
DR EMBL: X55008; CAB38245.2; -.
DR HSP: P00740; 1CFH.
DR InterPro: IPR000152; -.
DR InterPro: IPR000294; -.
DR InterPro: IPR000561; -.
DR InterPro: IPR000742; -.
DR InterPro: IPR001254; -.
DR InterPro: IPR001314; -.
DR InterPro: IPR001438; -.
DR InterPro: IPR001881; -.
DR InterPro: IPR002383; -.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00089; trypsin; 1.
DR Pfam: PF00594; g1a; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00010; EGFBL00D.
DR PRINTS: PR00001; GLABLO0D.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 456 AA; 51149 MW; 54E20A1B3964E234 CRC64;

Query Match 38.5%; Score 77; DB 4; Length 456;
Best Local Similarity 35.3%; Pred. No. 5.8e-05;
Matches 12; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 11 GSLKRCIXXICDPXAKXIFQNVDDTLAFWSKH 44
DB 53 GNLRECEMEKCSFEAREVENTERTTEFWKQY 86

RESULT 15

Q29094 PRELIMINARY; PRT; 648 AA.
AC Q29094;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE PROTEIN S (FRAGMENT).
GN PROS.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid=9823;

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RM [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LIVER:
RX MEDLINE-95134217; PubMed-7832752;
RA Greengard J.S., Fernandez J.A., Radtke K.P., Griffin J.H.;
RT *Identification of candidate residues for interaction of protein S
RT with Cab binding protein and activated protein C.*;
RL Blochem. J. 305:397-403(1995).
DR EMBL: L31379; AAA70382.1; -.
DR HSSP: P00740; ICFH.
DR InterPro: IPR00152; -.
DR InterPro: IPR000294; -.
DR InterPro: IPR000561; -.
DR InterPro: IPR001791; -.
DR InterPro: IPR001881; -.
DR InterPro: IPR002383; -.
DR Pfam: PF00008; EGF; 4.
DR Pfam: PF00054; Laminin_G; 1.
DR PRINTS: PR00001; GLABLOOD.
DR PROSITE: PS00010; ASX_HYDROXYL; 4.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 3.
DR PROSITE: PS01187; EGF_CA; 3.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR SMART: SM00282; LamG; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat;
KW Vitamin K.
FT NON_TER 1
SQ SEQUENCE 648 AA; 71914 MW; 4BDF9AB13872136 CRC64;
```

```
Query Match 37.5%; Score 75; DB 6; Length 648;
Best Local Similarity 36.6%; Pred. No. 0.00019;
Matches 15; Conservative 8; Mismatches 18; Indels 0; Gaps 0;
QY 1 ANSFLXLRHGSILRXICIXICDFFXXAKXIFQNVDDTLAFW 41
   ||| | : | | | | : | : | | : | |
DB 15 ANSMLEERKQGNLERECIEELCSKEAREVFNDEPETEFY 55
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Search completed: November 8, 2001, 08:55:54
Job time: 178 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 8, 2001, 08:53:16 ; Search time 9.93 Seconds

(without alignments)
151.787 Million cell updates/sec

Title: US-09-497-591-1

Perfect score: 200
Sequence: 1 ANSFLXLRHSGSLKRCIXX.....XXAKXIFQNVDDTLAFMSKH 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 3425486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	176	88.0	461	1 PRTC_HUMAN	P04070 homo sapien
2	147	73.5	461	1 PRTC_MOUSE	P33587 mus musculu
3	146	73.0	461	1 PRTC_RAT	P31394 rattus norv
4	141	70.5	458	1 PRTC_RABIT	Q28661 oryctolagus
5	129	64.5	456	1 PRTC_BOVIN	P00745 bos taurus
6	104	52.0	444	1 FA7_RABIT	P06139 oryctolagus
7	101	50.5	492	1 FA10_BOVIN	P00743 bos taurus
8	100	50.0	488	1 FA10_HUMAN	P00742 homo sapien
9	93	46.5	466	1 FA7_HUMAN	P08709 homo sapien
10	93	46.5	490	1 FA10_RABIT	O19045 oryctolagus
11	90	45.0	407	1 FA7_BOVIN	P22457 bos taurus
12	82.5	41.2	617	1 THRB_RAT	P18292 rattus norv
13	82.5	41.2	618	1 THRB_MOUSE	P18221 mus musculu
14	82	41.0	649	1 PRTS_MACMU	Q28520 macaca mlla
15	82	41.0	676	1 PRTS_HUMAN	P07225 homo sapien
16	81	40.5	452	1 FA9_CANFA	P19540 canis famli
17	81	40.5	459	1 FA9_MOUSE	P18294 mus musculu
18	81	40.5	646	1 PRTS_RABIT	P06118 oryctolagus
19	80	40.0	446	1 FA7_MOUSE	P70375 bos taurus
20	80	40.0	622	1 THRB_HUMAN	P00734 homo sapien
21	80	40.0	675	1 PRTS_BOVIN	P07224 bos taurus
22	78	39.0	675	1 PRTS_RAT	P5813 rattus norv
23	77	38.5	461	1 FA9_HUMAN	P00740 homo sapien
24	74	37.0	416	1 FA9_BOVIN	P00741 bos taurus
25	73	36.5	376	1 FA10_TROCA	P81428 tropicidnls
26	73	36.5	475	1 FA10_CHICK	P23155 gallus gall
27	71	35.5	675	1 PRTS_MOUSE	Q08761 mus musculu
28	68	34.0	625	1 THRB_BOVIN	P00735 bos taurus
29	65.5	32.8	400	1 PRTZ_HUMAN	P22891 homo sapien
30	59.5	29.8	396	1 PRTZ_BOVIN	P00744 bos taurus
31	53	28.5	501	1 MCOL_CANAL	P43068 candida alb
32	51	25.5	245	1 LDXP_VIRBA	P53300 vibrio harv
33	50	25.0	363	1 ADK_TOXGO	O9tww2 toxoplasma

ALIGNMENTS

RESULT 1	STANDARD:	PRT:	461 AA.
PRTC_HUMAN			
ID PRTC_HUMAN	016001; 015190; 015189;	PRT:	461 AA.
AC P04070; 016001; 015190; 015189;			
DT 01-NOV-1986 (Rel. 03, Created)			
DT 01-NOV-1986 (Rel. 03, Last sequence update)			
DT 01-OCT-2000 (Rel. 40, Last annotation update)			
DE VITAMIN-K DEPENDENT PROTEIN C PRECURSOR (EC 3.4.21.69)			
DE (AUTOPROTHROMBIN IIA) (ANTICOAGULANT PROTEIN C) (BLOOD COAGULATION			
DE FACTOR XIV).			
CM PROC.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX NCBI_Taxid:9606;			
[1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=85270390; PubMed=2991887;			
RA Foster D.C., Yoshitake S., Davie E.W.;			
RT "The nucleotide sequence of the gene for human protein C.;"			
RL Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677(1985).			
[2]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=85269639; PubMed=2991859;			
RA Beckmann R.J., Schmidt R.J., Santeiro R.F., Plutzky J., Crabtree G.R.,			
RL Long G.L.;			
RT "The structure and evolution of a 461 amino acid human protein C			
RT precursor and its messenger RNA, based upon the DNA sequence of			
RT cloned human liver cDNAs.;"			
RL Nucleic Acids Res. 13:5233-5247(1985).			
[3]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=86120978; PubMed=3511471;			
RA Plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.;			
RT "Evolution and organization of the human protein C gene.;"			
RL Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986).			
[4]			
RP SEQUENCE OF 106-461 FROM N.A.			
RX MEDLINE=84272714; PubMed=6589623;			
RA Foster D.C., Davie E.W.;			
RT "Characterization of a cDNA coding for human protein C.;"			
RL Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984).			
[5]			
RP CARBOHYDRATE-LINKAGE SITE ASN-371.			
RX MEDLINE=90293094; PubMed=1694179;			
RA Miletich J.P., Broze G.J. Jr.;			
RT "Beta protein C is not glycosylated at asparagine 329. The rate of			
RT translation may influence the frequency of usage at asparagine-X-			
RT cysteine sites.;"			
RL J. Biol. Chem. 265:11397-11404(1990).			
[6]			
RP HYDROXYLATION			
RX MEDLINE=92184750; PubMed=1544894;			
RA Harris R.J., Ling V.T., Spelman M.W.;			
RT "O-linked fucose is present in the first epidermal growth factor			
RT domain of factor XII but not protein C.;"			

34	49	24.5	422	1	SPM1_SCHPO	O92398 schizosacch
35	49	24.5	730	1	PRIA_HAETN	P44647 haemophilus
36	47.5	23.8	489	1	MEP3_YEAST	P53390 saccharomyc
37	47	23.5	467	1	VL2_HPV40	P36760 human papil
38	47	23.5	1333	1	VGRI_MOUSE	P35969 mus musculu
39	47	23.5	1336	1	VGRI_RAT	P33767 rattus norv
40	47	23.5	1338	1	VGRI_HUMAN	P17948 homo sapien
41	46	23.0	206	1	V930_HAETN	P44077 haemophilus
42	46	23.0	221	1	YHQO_ECOLI	P37619 escherichia
43	46	23.0	244	1	T2E5_ECOLI	P04390 escherichia
44	45.5	22.8	492	1	MEP1_YEAST	P40260 saccharomyc
45	44	22.0	372	1	B3G8_HUMAN	Q9y2a9 h probable

RL J. Biol. Chem. 267:5102-5107(1992).
RN [7]
RP 3D-STRUCTURE MODELING OF 175-450.
RX MEDLINE=94272342; PubMed=8003977;
RA Fisher C.L., Greengard J.S., Griffin J.H.;
RT "Models of the serine protease domain of the human antithrombotic
RT plasma factor activated protein C and its zymogen.";
RL Protein Sci. 3:588-599(1994).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 84-461.
RX MEDLINE=97157472; PubMed=9003757;
RA Mather T., Oganessyan V., Hof P., Huber R., Foundling S., Esmon C.,
RA Bode W.;
RT "The 2.8 A crystal structure of Gla-domainless activated protein C";
RL EMBO J. 15:6822-6831(1996).
RN [9]
RP REVIEW ON PROC VARIANTS.
RX MEDLINE=93190290; PubMed=8446940;
RA Reitsma P.H., Poort S.R., Bernardi F., Gandrille S., Long G.L.,
RA Sala N., Cooper D.N.;
RT "Protein C deficiency: a database of mutations. For the Protein C & S
RT Subcommittee of the Scientific and Standardization Committee of the
RT International Society on Thrombosis and Haemostasis.";
RL Thromb. Haemost. 69:77-84(1993).
RN [10]
RP VARIANT CYS-444.
RX MEDLINE=87204221; PubMed=2437584;
RA Romeo G., Hassan H.J., Staemfli S., Roncuzzi L., Cianetti L.,
RA Leonard A., Vicente V., Mannucci P.M., Bertina R., Peschle C.,
RA Cortese R.;
RT "Hereditary thrombophilia: identification of nonsense and missense
RT mutations in the protein C gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:2829-2832(1987).
RN [11]
RP VARIANT TRP-211 (LONDON-1).
RX MEDLINE=90089906; PubMed=2602169;
RA Grundy C., Chittoldi A., Talbot S., Bevan D., Kakkar V., Cooper D.N.;
RT "Protein C London 1: recurrent mutation at Arg-169 (CGG-->TGG) in
RT the protein C gene causing thrombosis.";
RL Nucleic Acids Res. 17:10513-10513(1989).
RN [12]
RP VARIANT CYS-272.
RX MEDLINE=91329836; PubMed=1866249;
RA Reitsma P.H., Poort S.R., Allart C.F., Briet E., Bertina R.M.;
RT "The spectrum of genetic defects in a panel of 40 Dutch families with
RT symptomatic protein C deficiency type I: heterogeneity and founder
RT effects.";
RL Blood 78:890-894(1991).
RN [13]
RP VARIANTS ALA-62 (VERMONT-1) AND MET-76.
RX MEDLINE=92190481; PubMed=1347706;
RA Bovill E.G., Tomczak J.A., Grant B., Bhushan F., Pillemer E.,
RA Rainville I.R., Long G.L.;
RT "Protein C Vermont: symptomatic type II protein C deficiency
RT associated with two Gla domain mutations.";
RL Blood 79:1456-1465(1992).
RN [14]
RP VARIANT ASP-418 (HONG KONG-2).
RX MEDLINE=92305321; PubMed=1611081;
RA Sugahara Y., Miura O., Yuen P., Aoki N.;
RT "Protein C deficiency Hong Kong 1 and 2: hereditary protein C
RT deficiency caused by two mutant alleles, a 5-nucleotide deletion and
RT a missense mutation.";
RL Blood 80:126-133(1992).
RN [15]
RP VARIANT LEU-289.
RX MEDLINE=92380660; PubMed=1511989;
RA Grundy C.B., Chisholm M., Kakkar V.V., Cooper D.N.;
RT "A novel homozygous missense mutation in the protein C (PROC) gene
RT causing recurrent venous thrombosis.";
RL Hum. Genet. 89:683-684(1992).
RN [16]
RP VARIANTS GLN-220 AND TRP-220.
RX MEDLINE=92380661; PubMed=1511989;
RA Grundy C.B., Schulman S., Tengborn L., Kakkar V.V., Cooper D.N.;
RT "Two different missense mutations at Arg 178 of the protein C (PROC)
RT gene causing recurrent venous thrombosis.";
RL Hum. Genet. 89:685-686(1992).
RN [17]
RP VARIANT GLN-220.
RX MEDLINE=93250852; PubMed=1301959;
RA Gandrille S., Vialaud M., Alach M., Alhenc-Gelas M., Fischer A.M.,
RA Gouault-Heilman M., Roulon P., Flessinger J.N., Goossens M.;
RT "Two novel mutations responsible for hereditary type I protein C
RT deficiency: characterization by denaturing gradient gel
RT electrophoresis.";
RL Hum. Mutat. 1:491-500(1992).
RN [18]
RP VARIANT SER-334.
RX MEDLINE=92276939; PubMed=1593215;
RA Yamamoto K., Matsushita T., Sugitara I., Takamatsu J., Iwaseki E.,
RA Wada H., Deguchi K., Shirakawa S., Saito H.;
RT "Homozygous protein C deficiency: identification of a novel missense
RT mutation that causes impaired secretion of the mutant protein C.";
RL J. Lab. Clin. Med. 119:682-689(1992).
RN [19]
RP VARIANTS TRP-38, CYS-42, HIS-42, GLN-271 AND ASN-294.
RX MEDLINE=93313192; PubMed=8324221;
RA Gandrille S., Alhenc-Gelas M., Gaussem P., Aillaud M.-F., Dupuy E.,
RA Jhan-Vague I., Alach M.;
RT "Five novel mutations located in exons III and IX of the protein C
RT gene in patients presenting with defective protein C anticoagulant
RT activity.";
RL Blood 82:159-168(1993).
RN [20]
RP VARIANTS G-14; Q-211; Y-244; Q-253; L-321; C-328; I-385; T-388; V-388.
RX MEDLINE=93271391; PubMed=8499565;
RA Poort S.R., Pabinger-Fasching I., Mannhalter C., Reitsma P.H.,
RA Bertina R.M.;
RT "Twelve novel and two recurrent mutations in 14 Austrian families
RT with hereditary protein C deficiency.";
RL Blood Coagul. Fibrinolysis 4:273-280(1993).
RN [21]
RP VARIANT TRP-57.
RX MEDLINE=93271396; PubMed=8499568;
RA Millar D.S., Grundy C.B., Bignelli P., Moffat E.H., Martin R.,
RA Kakkar V.V., Cooper D.N.;
RT "A Gla domain mutation (Arg 15-->Tyr) in the protein C (PROC) gene
RT causing type 2 protein C deficiency and recurrent venous
RT thrombosis.";
RL Blood Coagul. Fibrinolysis 4:345-347(1993).
RN [22]
RP VARIANTS R-145; L-210; W-211; T-243; L-321; M-340 AND Y-426.
RX MEDLINE=94122329; PubMed=8292730;
RA Tsay W., Greengard J.S., Montgomery R.R., McPherson R.A., Fucci J.C.,
RA Koepfer M.A., Coughlin J., Griffin J.H.;
RT "Genetic mutations in ten unrelated American patients with
RT symptomatic type I protein C deficiency.";
RL Blood Coagul. Fibrinolysis 4:791-796(1993).
RN [23]
RP VARIANT SER-423.
RX MEDLINE=94001606; PubMed=8398832;
RA Marchetti G., Patraccohni P., Gemmati D., Castaman G., Rodeghiero F.,
RA Wecey A., Cooper D.N., Tuddenham E.G., Bernardi F.;
RT "Symptomatic type II protein C deficiency caused by a missense
RT mutation (Gly 381-->Ser) in the substrate-binding pocket.";
RL Br. J. Haematol. 84:285-289(1993).
RN [24]
RP SEQUENCE OF 43-64 FROM N.A., AND VARIANT GLY-57 (YONAGO).
RX MEDLINE=93237511; PubMed=8477066;
RA Mimuro J., Muramatsu S., Kaneko M., Yoshitake S., Iijima K.,
RA Nakamura K., Sakata Y., Matsuda M.;
RT "An abnormal protein C (protein C Yonago) with an amino acid
RT substitution of Gly for Arg-15 caused by a single base mutation of C
RT to G in codon 57 (CGG-->GCG). Deteriorated calcium-dependent
RT conformation of the gamma-carboxyglutamic acid domain relevant to a


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FT DISULFID 161 174 BY SIMILARITY.
FT DISULFID 182 319 INTERCHAIN (BY SIMILARITY).
FT DISULFID 238 254 BY SIMILARITY.
FT DISULFID 373 387 BY SIMILARITY.
FT DISULFID 398 426 BY SIMILARITY.
FT CARBOHYD 214 214 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 328 328 MISSING (IN REF. 2).
FT CONFLICT 393 393 N -> D (IN REF. 2).
SQ SEQUENCE 461 AA; 51945 MW; 53FA0D85B194D6E CRC64;

Query Match 73.5%; Score 147; DB 1; Length 461;
Best Local Similarity 63.6%; Pred. No. 3.1e-17;
Matches 28; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

OY 1 ANSLXLRHSGSLKXCLXXICDPXKXKXIFQNDPLAFMSKH 44
DB 42 ANSLXLRHSGSLKXCLXXICDPXKXKXIFQNDPLAFMSKH 85

RESULT 3
PRIC_RAT STANDARD; PRT: 461 AA.
ID PRIC_RAT
AC P31394;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE VITAMIN-K DEPENDENT PROTEIN C PRECURSOR (EC 3.4.21.69)
DE (AUTOPROTHROMBIN IIA) (ANTICOAGULANT PROTEIN C) (BLOOD COAGULATION
DE FACTOR XIV).
GN PROC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus;
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WISTAR; TISSUE=Liver;
RX MEDLINE=92329550; PubMed=1627650;
RA Okafuji T., Maekawa K., Nawa K., Marumoto Y.;
RL Blochlm. Biophys. Acta 1131:329-332(1992).
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: DEGRADATION OF BLOOD COAGULATION FACTORS VA
CC AND VIIIA.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC GU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC -----
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AC P00745;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE VITAMIN-K DEPENDENT PROTEIN C PRECURSOR (EC 3.4.21.69)
 DE (AUTOPROTHROMBIN IIA) (ANTICOAGULANT PROTEIN C) (BLOOD COAGULATION
 DE FACTOR XIV) (FRAGMENT).
 GN PROC.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID:9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85014826; PubMed=6091100;
 RA Long G.L., Balagaje R.M., McGillivray R.T.A.;
 RT "Cloning and sequencing of liver cDNA coding for bovine protein C.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).
 RN [2]
 RP SEQUENCE OF 40-194.
 RX MEDLINE=83007325; PubMed=6896876;
 RA Fernlund P., Stenflo J.;
 RT "Amino acid sequence of the light chain of bovine protein C.";
 RL J. Biol. Chem. 257:12170-12179(1982).
 RN [3]
 RP REVISION TO 110.
 RX MEDLINE=83169769; PubMed=6572939;
 RA Drakenberg T., Fernlund P., Roepstorff P., Stenflo J.;
 RT "beta-hydroxyaspartic acid in vitamin K-dependent protein C.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).
 RN [4]
 RP SEQUENCE OF 197-456.
 RX MEDLINE=83007326; PubMed=6896877;
 RA Stenflo J., Fernlund P.;
 RT "Amino acid sequence of the heavy chain of bovine protein C.";
 RL J. Biol. Chem. 257:12180-12190(1982).
 RN [5]
 RP PROCESSING, AND CALCIUM-BINDING DATA.
 RX MEDLINE=83213513; PubMed=6304092;
 RA Esmon N.L., Debault L.E., Esmon C.T.;
 RT "Proteolytic formation and properties of gamma-carboxyglutamic acid-
 RT domainless protein C.";
 RL J. Biol. Chem. 258:5548-5553(1983).
 RN [6]
 RP PROCESSING, AND CALCIUM-BINDING DATA.
 RX MEDLINE=83213514; PubMed=6406503;
 RA Johnson A.F., Esmon N.L., Laue T.M., Esmon C.T.;
 RT "Structural changes required for activation of protein C are induced
 RT by Ca2+ binding to a high affinity site that does not contain gamma-
 RT carboxyglutamic acid.";
 RL J. Biol. Chem. 258:5554-5560(1983).
 CC - FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
 CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
 CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
 CC - CATALYTIC ACTIVITY: DEGRADATION OF BLOOD COAGULATION FACTORS VA
 CC AND VIIIA.
 CC - SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
 CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
 CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
 CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN. THIS
 CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
 CC STRONGLY PROMOTED BY THROMBOMODULIN.
 CC - TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
 CC - PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
 CC - MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
 CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
 CC THROMBIN-THROMBOMODULIN COMPLEX.
 CC - SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.

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 DR EMBL: K02435; AAA30685.1; -
 DR PIR: A00928; KXBO.
 DR HSSP: P04070; 1AOT.
 DR MEROPS: S01.218; -
 DR InterPro: IPR000152; -
 DR InterPro: IPR000294; -
 DR InterPro: IPR000561; -
 DR InterPro: IPR001254; -
 DR InterPro: IPR001881; -
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00594; gla; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_CA; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; FALSE_NEG.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Blood coagulation; Glycoprotein; Plasma; Serine protease; Liver;
 KW gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 KW EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 29
 FT PROPEP 30 39
 FT CHAIN 40 194
 FT CHAIN 197 456
 FT PEPTIDE 197 210
 FT DOMAIN 94 129
 FT DOMAIN 133 173
 FT DOMAIN 211 456
 FT MOD_RES 45 45
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 FT MOD_RES 110 110
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 FT ACT_SITE 298 298
 FT ACT_SITE 397 397
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 FT DISULFID 89 108
 FT DISULFID 98 103
 FT DISULFID 102 117
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 FT DISULFID 137 148
 FT DISULFID 144 157
 FT DISULFID 159 172
 FT DISULFID 180 318
 FT DISULFID 237 253
 FT DISULFID 368 382
 FT DISULFID 393 421
 FT CARBOHYD 136 136
 FT CARBOHYD 289 289
 FT CARBOHYD 350 350
 FT CARBOHYD 366 366
 FT VARIANT 82 82
 FT CONFLICT 455 456
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 N-LINKED (GLCNAC. . .)
 N-LINKED (GLCNAC. . .)
 N-LINKED (GLCNAC. . .)
 N-LINKED (GLCNAC. . .)
 F -> K.
 VP -> PV (IN REF. 4).

ID FA10_BOVIN STANDARD; PRT; 492 AA.
AC P00743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE COAGULATION FACTOR X PRECURSOR (EC 3.4.21.6) (STUART FACTOR).
GN F10.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE OF 1-487 FROM N.A.
RX MEDLINE=84247315; PubMed=6330671;
RA Fung M.R., Campbell R.M., McGilivray R.T.A.;
RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
RT containing a prepro leader sequence.";
RL Nucleic Acids Res. 12:4481-4492(1984).
RN [2]
RP SEQUENCE OF 41-180.
RX MEDLINE=80130563; PubMed=6766735;
RA Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
RA Titani K.;
RT "Amino acid sequence of the light chain of bovine factor XI (Stuart
RT factor).";
RL Biochemistry 19:659-667(1980).
RN [3]
RP REVISION TO 103.
RX MEDLINE=83308813; PubMed=6688526;
RA McMullen B.A., Fujikawa K., Kistiel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
RT K-dependent blood coagulation zymogens.";
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN [4]
RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX MEDLINE=7603066; PubMed=1059093;
RA Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
RA Neurath H.;
RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
RT chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
RN [5]
RP SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=94062825; PubMed=8243461;
RA Inoue K., Morita T.;
RT "Identification of O-linked oligosaccharide chains in the activation
RT peptides of blood coagulation factor X. The role of the carbohydrate
RT moieties in the activation of factor X.";
RL Eur. J. Biochem. 218:153-163(1993).
RN [6]
RP ACTIVE SITE.
RX MEDLINE=73053314; PubMed=4264286;
RA Titani K., Hermanson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
RA Neurath H., Davie E.W.;
RT "Bovine factor XIa (activated Stuart factor). Evidence of homology
RT with mammalian serine proteases.";
RL Biochemistry 11:4899-4903(1972).
RN [7]
RP PROCESSING.
RX MEDLINE=76053121; PubMed=1059122;
RA Fujikawa K., Titani K., Davie E.W.;
RT "Activation of bovine factor X (Stuart factor): conversion of factor
RT Xa-alpha to factor Xa-beta.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
RN [8]
RP CALCIUM-BINDING DATA.
RX MEDLINE=84185716; PubMed=6546930;
RA Sugo T., Björck I., Holmgren A., Stenflo J.;
RT "Calcium-binding properties of bovine factor X lacking the gamma-
RT carboxyglutamic acid-containing region.";
RL J. Biol. Chem. 259:5705-5710(1984).
RN [9]

RP SULFATE-BINDING.
RX MEDLINE=86140210; PubMed=3949800;
RA Morita T., Jackson C.M.;
RT "Localization of the structural difference between bovine blood
RT coagulation factors XI and X2 to tyrosine 18 in the activation
RT peptide.";
RL J. Biol. Chem. 261:4008-4014(1986).
RN [10]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=91084483; PubMed=261466;
RA Selander M., Persson E., Stenflo J., Drakenberg T.;
RT "1H NMR assignment and secondary structure of the Ca2(+)-free form of
RT the amino-terminal epidermal growth factor like domain in coagulation
RT factor X.";
RL Biochemistry 29:8111-8118(1990).
RN [11]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=92329412; PubMed=1627540;
RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
RA Telman O.;
RT "Three-dimensional structure of the apo form of the N-terminal
RT EGF-like module of blood coagulation factor X as determined by NMR
RT spectroscopy and simulated folding.";
RL Biochemistry 31:5974-5983(1992).
RN [12]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=92406922; PubMed=1527084;
RA Selander M., Ullner M., Persson E., Telman O.,
RA Stenflo J., Drakenberg T.;
RT "How an epidermal growth factor (EGF)-like domain binds calcium. High
RT resolution NMR structure of the calcium form of the NH2-terminal EGF-
RT like domain in coagulation factor X.";
RL J. Biol. Chem. 267:19642-19649(1992).
RN [13]
RP STRUCTURE BY NMR OF 41-126.
RX MEDLINE=96387194; PubMed=8794734;
RA Sunnerhagen M., Olaf G.A., Stenflo J., Forsen S., Drakenberg T.,
RA Tremella J.;
RT "The relative orientation of Gla and EGF domains in coagulation
RT factor X is altered by Ca2+ binding to the first EGF domain. A
RT combined NMR-small angle X-ray scattering study.";
RL Biochemistry 35:11547-11559(1996).
RN [14]
RP FUNCTION: FACTOR XA IS A VITAMIN K-DEPENDENT GLYCOPROTEIN THAT
CC CONVERTS PROTHROMBIN TO THROMBIN IN THE PRESENCE OF FACTOR VA,
CC CA2+, AND PHOSPHOLIPID DURING BLOOD CLOTTING.
CC [1-] CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-1-THR AND THEN
CC ARG-1-THE BONDS IN PROTHROMBIN TO FORM THROMBIN.
CC [1-] SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
CC MORE DISULFIDE BONDS.
CC [1-] PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM.
CC [1-] PTM: N- AND O-GLYCOSYLATED.
CC [1-] PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
CC [1-] MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN.
CC [1-] SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC [1-] SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC -----
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CC -----
DR EMBL: X00673; CAA25286.1; -
DR PIR: A00925; EXBO.
DR PDB: IABO; 3I-JAN-94.

DR PDB: 1CCE; 31-MAY-94.
DR PDB: 1WHE; 15-MAY-97.
DR PDB: 1WHF; 15-MAY-97.
DR MEROPS: S01.216; -.
DR GlycoSuiteDB: P00743; -.
DR Carbank; CCSD:7747; -.
DR Carbank; CCSD:7899; -.
DR Carbank; CCSD:11506; -.
DR Carbank; CCSD:11508; -.
DR InterPro: IPR00152; -.
DR InterPro: IPR00294; -.
DR InterPro: IPR00561; -.
DR InterPro: IPR001254; -.
DR InterPro: IPR001314; -.
DR InterPro: IPR001881; -.
DR InterPro: IPR002383; -.
DR Pfam: PF00008; EGF 2.
DR Pfam: PF00594; g1a; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00001; GLABLOOD.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
KW Gamma-Carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
KW Signal; Zymogen; EGF-like domain; Repeat; 3D-structure.
FT SIGNAL 1 40
FT PROPEP 1 40
FT CHAIN 41 180
FT CHAIN 183 492
FT PROPEP 183 233
FT CHAIN 234 492
FT PROPEP 476 492
FT DOMAIN 86 122
FT DOMAIN 125 165
FT DOMAIN 234 492
FT MOD_RES 46 46
FT MOD_RES 47 47
FT MOD_RES 54 54
FT MOD_RES 55 56
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FT MOD_RES 65 65
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FT MOD_RES 69 69
FT MOD_RES 72 72
FT MOD_RES 75 75
FT MOD_RES 79 79
Query Match 50.5%; Score 101; DB 1; Length 492;
Best Local Similarity 38.6%; Pred. No. 2,1e-09;
Matches 17; Conservative 10; Mismatches 17; Indels 0; Gaps 0;
OY 1 ANSLFXLRHSLKRXCLXICDFYXAKXIFONVDDTLAFWSKH 44
DB 41 ANSLFLEVKQCNLERECLEACSLSEAREVFEDAQOTDEFWSKY 84

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91216473; PubMed=1902434;
RA Messier T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;
RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding
human coagulation factor X.";
RL Gene 99:291-294(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=67026600; PubMed=3768336;
RA Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;
RT "Gene for human factor X: a blood coagulation factor whose gene
organization is essentially identical with that of factor IX and
protein C.";
RL Biochemistry 25:5098-5102(1986).
RN [3]
RP SEQUENCE OF 13-488 FROM N.A.
RX MEDLINE=65216545; PubMed=2582420;
RA Fung M.R., Hay C.W., McGillivray R.T.A.;
RT "Characterization of an almost full-length cDNA coding for human
blood coagulation factor X.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
RN [4]
RP SEQUENCE OF 19-488 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=86221713; PubMed=3011603;
RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
RT "Isolation and characterization of human blood-coagulation factor X
cDNA.";
RL Gene 41:311-314(1986).
RN [5]
RP SEQUENCE OF 41-179.
RX MEDLINE=63257207; PubMed=6871167;
RA Mcullen B.A., Fujikawa K., Kisiel W., Sasagawa T., Howald W.N.,
Kwa E.Y., Weinstein B.;
RT "Complete amino acid sequence of the light chain of human blood
coagulation factor X: evidence for identification of residue 63 as
beta-hydroxyaspartic acid.";
RL Biochemistry 22:2875-2884(1983).
RN [6]
RP SEQUENCE OF 115-488 FROM N.A.
RX MEDLINE=84222026; PubMed=6587384;
RA Leytus S.P., Chung D.W., Kisiel W., Kurachi K., Davie E.W.;
RT "Characterization of a cDNA coding for human factor X.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).
RN [7]
RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=94062825; PubMed=8243461;
RA Inoue K., Morita T.;
RT "Identification of O-linked oligosaccharide chains in the activation
peptides of blood coagulation factor X. The role of the carbohydrate
moieties in the activation of factor X.";
RL Eur. J. Biochem. 218:153-163(1993).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.
RX MEDLINE=93360277; PubMed=8355279;
RA Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W.,
Huber R., Blankenship D.T., Cardin A.D., Kisiel W.;
RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";
RL J. Mol. Biol. 232:947-966(1993).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
RX MEDLINE=98283982; PubMed=9618463;
RA Kamata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;
RT "Structural basis for chemical inhibition of human blood coagulation
factor Xa.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).
CC -1- FUNCTION: FACTOR XA IS A VITAMIN K-DEPENDENT GLYCOPROTEIN THAT
CONVERTS PROTHROMBIN TO THROMBIN IN THE PRESENCE OF FACTOR VA,

CC CA++ AND PHOSPHOLIPID DURING BLOOD CLOTTING.
 CC -1- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-|-THR AND THEN
 CC ARG-|-ILE BONDS IN PROTHROMBIN TO FORM THROMBIN.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -1- PTM: N- AND O-GLYCOSYLATED.
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
 CC -1- SIMILARITY: CONTRAINS 2 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC -----
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 CC -----
 CC EMBL: K03194; AAA52490.1; -;
 CC EMBL: M57285; AAA52421.1; -;
 CC EMBL: L29433; AAA52764.1; -;
 CC EMBL: L00390; AAA52764.1; JOINED.
 CC EMBL: L00391; AAA52764.1; JOINED.
 CC EMBL: L00392; AAA52764.1; JOINED.
 CC EMBL: L00393; AAA52764.1; JOINED.
 CC EMBL: L00394; AAA52764.1; JOINED.
 CC EMBL: L00395; AAA52764.1; JOINED.
 CC EMBL: L00396; AAA52764.1; JOINED.
 CC EMBL: M22613; AAA51984.1; -;
 CC PIR: A00924; EXHU.
 CC PIR: A25853; A25853.
 CC PIR: A24478; A24478.
 CC PDB: 1HCG; 08-MAY-95.
 CC PDB: 1FAX; 29-OCT-97.
 CC PDB: 1FXY; 17-JUN-98.
 CC PDB: 1XKA; 23-MAR-99.
 CC PDB: 1XKB; 23-MAR-99.
 CC MEROPS; S01.216; -;
 CC DR GlycosultedB: P00742; -;
 CC DR Carbank; CCSD: 29393; -;
 CC DR MIM: 134530; -;
 CC DR InterPro: IPR000152; -;
 CC DR InterPro: IPR000294; -;
 CC DR InterPro: IPR000561; -;
 CC DR InterPro: IPR001254; -;
 CC DR InterPro: IPR001314; -;
 CC DR InterPro: IPR001881; -;
 CC DR InterPro: IPR002383; -;
 CC DR Pfam: PF00008; EGF_2.
 CC DR Pfam: PF00594; g1a_1.
 CC DR Pfam: PF00089; trypsin_1.
 CC DR PRINTS: PR00001; GLABLOOD.
 CC DR PRINTS: PR00722; CHYMOTRYPSIN.
 CC DR PROSITE: PS00010; ASX-HYDROXYL; 1.
 CC DR PROSITE: PS00011; GLU-CARBOXYLATION; 1.
 CC DR PROSITE: PS00022; EGF_1; 1.
 CC DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 CC DR PROSITE: PS00135; TRYPSIN_SER; 1.
 CC DR PROSITE: PS01186; EGF_2; 2.
 CC DR PROSITE: PS01187; EGF_CA; 1.
 CC KW Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
 CC Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 CC Signal; Zymogen; EGF-like domain; Repeat; 3D-structure.
 CC FT SIGNAL 1 40
 CC FT PROPEP 1 40
 CC FT CHAIN 41 179 FACTOR X LIGHT CHAIN.

FT CHAIN 183 488 FACTOR X HEAVY CHAIN.
 FT PROPEP 183 234 ACTIVATION PEPTIDE.
 FT CHAIN 235 488 ACTIVATED FACTOR XA, HEAVY CHAIN.
 FT DOMAIN 86 122 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 125 165 EGF-LIKE 2.
 FT DOMAIN 235 488 CATALYTIC.
 FT MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 55 56 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
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 FT MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 103 103 GAMMA-CARBOXYGLUTAMIC ACID.
 FT CARBOHYD 199 199
 FT CARBOHYD 211 211
 FT CARBOHYD 221 221
 FT CARBOHYD 231 231
 FT ACT_SITE 276 276
 FT ACT_SITE 322 322
 FT ACT_SITE 419 419
 FT ACT_SITE 90 101
 FT DISULFID 95 110
 FT DISULFID 112 121
 FT DISULFID 129 140
 FT DISULFID 136 149
 FT DISULFID 151 164
 FT DISULFID 172 342
 FT DISULFID 241 246
 FT DISULFID 261 277
 FT DISULFID 390 404
 FT DISULFID 415 443
 FT CONFLICT 285 288
 FT CONFLICT 442 442
 FT SEQUENCE 488 AA; 54731 MW; F81D5746AF4797AF CRC64;
 KRVV -> E (IN REF. 4 AND 6).
 G -> S (IN REF. 3).
 F81D5746AF4797AF CRC64;
 Query Match 50.0%; Score 100; DB 1; Length 488;
 Best Local Similarity 38.6%; Pred. No. 3; Le-09;
 Matches 17; Conservative 10; Mismatches 17; Indels 0; Gaps 0;
 QY 1 ANSEFLXLRHGSIXKXCIXXICDFXXAKXIFQVNDPLAFMSKH 44
 DB 41 ANSEFLXMKKXHLERECMEETCSYEAREVFEEDSDKINERWNY 84
 RESULT 9
 ID FA7_HUMAN STANDARD; PRT; 466 AA.
 AC P08709;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE COAGULATION FACTOR VII PRECURSOR (BC 3.4.21.21) (SERUM PROTHROMBIN
 DE CONVERSION ACCELERATOR) (EPTACOG ALFA).
 GN F7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86205965; PubMed=3486420;
 RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,
 RA Woodbury R.G., Hart C.E., Insley M.Y., Kistiel W., Kutachi K.,
 RA Davie E.W.;
 RT "Characterization of a cDNA coding for human factor VII.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
 RN [2]

RP SEQUENCE FROM N.A.
RX MEDLINE-87260948; PubMed-3037537;
RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,
HA Hagen F.S., Murray M.J.;
RT "Nucleotide sequence of the gene coding for human factor VII, a
RT vitamin K-dependent protein participating in blood coagulation.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
RN [13]
RP SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE-89088153; PubMed-3264725;
RA Thim L., Bjoern S., Christensen M., Nicolaisen E.M., Lund-Hansen T.,
RA Pederesen A.H., Hedner U.;
RT "Amino acid sequence and posttranslational modifications of human
RT factor VIIa from plasma and transfected baby hamster kidney cells.";
RL Biochemistry 27:7785-7793(1988).
RN [14]
RP CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
RX MEDLINE-91250411; PubMed-1904059;
RA Bjoern S., Foster D.C., Thim L., Wlberg F.C., Christensen M.,
RA Komlyama Y., Pederesen A.H., Kistiel W.;
RT "Human plasma and recombinant factor VII. Characterization of O-
RT glycosylations at serine residues 52 and 60 and effects of site-
RT directed mutagenesis of serine 52 to alanine.";
RL J. Biol. Chem. 266:11051-11057(1991).
RN [15]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE-90062160; PubMed-2511201;
RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,
RA Shimonishi Y., Iwanaga S.;
RT "Identification of a disaccharide (xy1-Glc) and a trisaccharide
RT (xy12-Glc) O-glycosidically linked to a serine residue in the first
RT epidermal growth factor-like domain of human factors VII and IX and
RT protein Z and bovine protein Z.";
RL J. Biol. Chem. 264:20320-20325(1989).
RN [16]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE-91344709; PubMed-2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the
RT first EGF-like domain of clotting factors VII and IX and protein Z";
RL Adv. Exp. Med. Biol. 281:121-131(1990).
RN [17]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
RX MEDLINE-96175641; PubMed-8598903;
RA Banner D.W., D'Arcy A., Chene C., Munkler F.K., Guha A.,
RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;
RT "The crystal structure of the complex of blood coagulation factor
RT VIIa with soluble tissue factor.";
RL Nature 380:41-46(1996).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
RX MEDLINE-99126538; PubMed-9925787;
RA Zhang E., St. Charles R., Tulinsky A.;
RT "Structure of extracellular tissue factor complexed with factor VIIa
RT inhibited with a BPTI mutant.";
RL J. Mol. Biol. 285:2089-2104(1999).
RN [19]
RP STRUCTURE BY NMR OF 105-145.
RX MEDLINE-98367502; PubMed-9692950;
RA Mutsaers J.A., Finn B.E., Glibert G.P., Forsen S., Stenflo J.,
RA Drekenberg T.;
RT "Solution structure of the N-terminal EGF-like domain from human
RT factor VII.";
RL Biochemistry 37:10605-10615(1998).
RN [10]
RP VARIANT GLN-364.
RX MEDLINE-91300046; PubMed-2070047;
RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
RA Meade T.W., Tuddenham E.G.D.;
RT "Purification and characterization of factor VII 304-Gln: a variant
RT molecule with reduced activity isolated from a clinically unaffected
RT male.";
RL Blood 78:132-140(1991).
RN [11]
RP VARIANTS GLN-364 AND PHE-370.
RX MEDLINE-92340074; PubMed-1634227;
RA Marchetti G., Patraccchini P., Gemmati D., Derosa V., Pinotti M.,
RA Rodorigo G., Casanato A., Girolami A., Bernardi F.;
RT "Detection of two missense mutations and characterization of a repeat
RT polymorphism in the factor VII gene (F7).";
RL Hum. Genet. 89:497-502(1992).
RN [12]
RP VARIANT TYR-238.
RX MEDLINE-93378811; PubMed-8364544;
RA Marchetti G., Ferrari M., Patraccchini P., Redaelli R., Bernardi F.;
RT "A missense mutation (178Cys->Tyr) and two neutral dimorphisms
RT (115His and 333Ser) in the human coagulation factor VII gene.";
RL Hum. Mol. Genet. 2:1055-1056(1993).
RN [13]
RP VARIANTS.
RX MEDLINE-94061028; PubMed-8242057;
RA Takamiya O., Kempall-Cook G., Marin D.M.A., Cooper D.N.,
RA von Felten A., Mell E., Hahn I., Prangnell D.R., Lunley H.,
RA Tuddenham E.G.D., McVey J.H.;
RT "Detection of missense mutations by single-strand conformational
RT polymorphism (SSCP) analysis in five dysfunctional variants of
RT coagulation factor VII.";
RL Hum. Mol. Genet. 2:1355-1359(1993).
RN [14]
RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.
RX MEDLINE-94264305; PubMed-8204879;
RA Chaiing S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,
RA Roberts H.R., Blaschman M., Monroe D.M., High K.A.;
RT "Severe factor VII deficiency caused by mutations abolishing the
RT cleavage site for activation and altering binding to tissue factor.";
RL Blood 83:3524-3535(1994).
RN [15]
RP VARIANT VAL-354.
RX MEDLINE-95072589; PubMed-7981691;
RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,
RA Rodeghiero F., Marchetti G.;
RT "Topologically equivalent mutations causing dysfunctional coagulation
RT factors VII (294Ala->Val) and X (334Ser->Pro).";
RL Hum. Mol. Genet. 3:1175-1177(1994).
RN [16]
RP VARIANT MIE HIS-307.
RX MEDLINE-95064662; PubMed-7974346;
RA Ohlwa M., Hayashi T., Mada H., Minamikawa K., Shitakawa S.,
RA Suzuki K.;
RT "Factor VII Mle: homozygous asymptomatic type I deficiency caused by
RT an amino acid substitution of His (CAC) for Arg(247) (CGC) in the
RT catalytic domain.";
RL Thromb. Haemost. 71:773-777(1994).
RN [17]
RP VARIANT MET-419.
RX MEDLINE-96247510; PubMed-8652821;
RA Arbini A.A., Mannucci P.M., Bauer K.A.;
RT "A Thr359Met mutation in factor VII of a patient with a hereditary
RT deficiency causes defective secretion of the molecule.";
RL Blood 87:5085-5094(1996).
RN [18]
RP VARIANTS W-283; K-325; V-358; Q-364; E-402 AND Q-413.
RX MEDLINE-97001216; PubMed-8844208;
RA Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,
RA Lunghi B., Rodeghiero F., Marchetti G.;
RT "Mutation pattern in clinically asymptomatic coagulation factor VII
RT deficiency.";
RL Hum. Mutat. 8:108-115(1996).
RN [19]
RP VARIANT VAL-304.
RX MEDLINE-97037613; PubMed-8883260;
RA Tanary H., Fromovich Y., Salmon L., Reich Z., Dym O., Lanir N.,
RA Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M.,
RA Zaitov R., Seligson U.;
RT "Ala244Val is a common, probably ancient mutation causing factor VII
RT deficiency in Moroccan and Iranian Jews.";

```

RL   Thromb. Haemost. 76:283-291(1996).
RN   [20]
RP   VARIANT(S) MALTA THR-194 AND VAL-304.
RA   MEDLINE=96112461; Pubmed=9452082;
RX   Alshinawi C., Seceri C., Galdies R., Aguilina A., Felice A.E.;
RT   "Two new missense mutations (P134T and A244V) in the coagulation
RT   factor VII gene.";
RL   Hum. Mutat. Suppl. 1:S189-S191(1998).
CC   -I- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
CC   CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR
CC   THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
CC   AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA
CC   BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO
CC   FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
CC   -I- CATALYTIC ACTIVITY: HYDROLYSES ONE ARG-|-ILE BOND IN FACTOR X TO
CC   FORM FACTOR XA.
CC   -I- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC   BY A DISULFIDE BOND.
CC   -I- TISSUE SPECIFICITY: PLASMA.
CC   -I- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC   GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC   CALCIUM.
CC   -I- DISEASE: DEFECTS IN F7 CAN CAUSE COAGULOPATHY.
CC   -I- PHARMACEUTICAL: AVAILABLE UNDER THE NAMES NISTASE OR NOVOSEVEN
CC   (NOVO NORDISK). USED FOR THE TREATMENT OF BLEEDING EPISODES IN
CC   HEMOPHILIA A OR B PATIENTS WITH ANTIBODIES TO COAGULATION FACTORS
CC   VIII OR IX.
CC   -I- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC   -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE
CC   TRYPSIN FAMILY.
CC   -I- DATABASE: NAME=Factor VII mutation database;
CC   WWW="http://europa.mmc.frms.ac.uk/usf/www/webpages/FVII/database.dlr/tilepage
CC   -----
Query Match          46.5%; Score 93; DB 1; Length 466;
Best Local Similarity 46.3%; Pred. NO. 4.5e-08;
Matches 19; Conservative 5; Mismatches 17; Indels 0; Gaps 0;
OY   1 ANSFLLXLRHGSGLKRXCLIXTCDFXXAKXIFQNVDDTLAFW 41
      ||||| ||||| | | | : || : | ||
DB   61 ANAFLEELRPGSLERECKEEQCSEAREEIFKDAERTKLFW 101
RESULT 10
FA10_RABIT
ID   FA10_RABBIT STANDARD. PRT. 490 AA.
AC   O19045;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DE   15-DEC-1998 (Rel. 37, Last annotation update)
DE   COAGULATION FACTOR X PRECURSOR (EC 3.4.21.6) (STUART FACTOR).
GN   F10.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_Taxid=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97256311; Pubmed=9101642;
RT   Peduruthi U.R., Anderson K.D., James H.L.;
RL   "Characterization of a full-length cDNA for rabbit factor X.";
RL   Thromb. Res. 85:503-514(1997).
CC   -I- FUNCTION: FACTOR XA IS A VITAMIN K-DEPENDENT GLYCOPROTEIN THAT
CC   CONVERTS PROTHROMBIN TO THROMBIN IN THE PRESENCE OF FACTOR VA,
CC   CA++ , AND PHOSPHOLIPID DURING BLOOD CLOTTING.
CC   -I- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-|-THR AND THEN
CC   ARG-|-ILE BONDS IN PROTHROMBIN TO FORM THROMBIN.
CC   -I- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
CC   BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
CC   MORE DISULFIDE BONDS.
CC   -I- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC   GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC   CALCIUM (BY SIMILARITY).

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CC	-1	PM: N- AND O-GLYCOSYLATED (BY SIMILARITY).		
CC	-1	PM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE		
CC	-1	INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)		
CC	-1	(BY SIMILARITY).		
CC	-1	MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO		
CC	-1	ANOTHER SITE, BEYOND THE GLA DOMAIN.		
CC	-1	SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.		
CC	-1	SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE		
CC	-1	TRIPSPIN FAMILY.		
CC	-1	-----		
CC	-1	THIS SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	-1	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	-1	the European Bioinformatics Institute. There are no restrictions on its		
CC	-1	use by non-profit institutions as long as its content is in no way		
CC	-1	modified and this statement is not removed. Usage by and for commercial		
CC	-1	entities requires a license agreement (see http://www.isb-sib.ch/announce/		
CC	-1	or send an email to license@isb-sib.ch).		
CC	-1	-----		
DR	EMBL; AF003200; AAB62542.1; -			
DR	InterPro; IPR000152; -			
DR	InterPro; IPR000294; -			
DR	InterPro; IPR000561; -			
DR	InterPro; IPR001254; -			
DR	InterPro; IPR001314; -			
DR	InterPro; IPR001881; -			
DR	InterPro; IPR002383; -			
DR	Pfam; PF00008; EGF; 2.			
DR	Pfam; PF00594; gla; 1.			
DR	Pfam; PF00089; trypsin; 1.			
DR	PRINTS; PR00001; GLABLOOD.			
DR	PRINTS; PR00722; CHYMOTRYPSIN.			
DR	PROSITE; PS00010; ASX_HYDROXYL; 1.			
DR	PROSITE; PS00011; GLU_CARBOXYLATION; 1.			
DR	PROSITE; PS00022; EGF_1; 1.			
DR	PROSITE; PS01186; EGF_2; 2.			
DR	PROSITE; PS01187; EGF_CA; 1.			
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.			
DR	PROSITE; PS00135; TRYPSIN_SER; 1.			
KW	Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;			
KW	Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;			
KW	Signal; Zymogen; EGF-like domain; Repeat.			
FT	SIGNAL	1	20	POTENTIAL.
FT	PROPEP	21	40	BY SIMILARITY.
FT	CHAIN	41	180	FACTOR X LIGHT CHAIN.
FT	CHAIN	184	490	FACTOR X HEAVY CHAIN.
FT	PROPEP	184	232	ACTIVATION PEPTIDE.
FT	CHAIN	233	490	ACTIVATED FACTOR XA, HEAVY CHAIN.
FT	DOMAIN	86	122	EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	125	165	EGF-LIKE 2.
FT	DOMAIN	233	490	CATALYTIC.
FT	MOD_RES	46	46	GAMMA-CARBOXYGLUTAMIC ACID (BY
FT	MOD_RES	47	47	SIMILARITY).
FT	MOD_RES	47	47	GAMMA-CARBOXYGLUTAMIC ACID (BY
FT	MOD_RES	54	54	SIMILARITY).
FT	MOD_RES	54	54	GAMMA-CARBOXYGLUTAMIC ACID (BY
FT	MOD_RES	56	56	SIMILARITY).
FT	MOD_RES	56	56	GAMMA-CARBOXYGLUTAMIC ACID (BY
FT	MOD_RES	59	59	SIMILARITY).
FT	MOD_RES	59	59	GAMMA-CARBOXYGLUTAMIC ACID (BY
FT	MOD_RES	60	60	SIMILARITY).
FT	MOD_RES	60	60	GAMMA-CARBOXYGLUTAMIC ACID (BY
FT	MOD_RES	65	65	SIMILARITY).
FT	MOD_RES	65	65	GAMMA-CARBOXYGLUTAMIC ACID (BY
FT	MOD_RES	66	66	SIMILARITY).
FT	MOD_RES	66	66	GAMMA-CARBOXYGLUTAMIC ACID (BY
FT	MOD_RES	69	69	SIMILARITY).
FT	MOD_RES	69	69	GAMMA-CARBOXYGLUTAMIC ACID (BY
FT	MOD_RES	72	72	SIMILARITY).
FT	MOD_RES	72	72	GAMMA-CARBOXYGLUTAMIC ACID (BY
FT	MOD_RES	75	75	SIMILARITY).
FT	MOD_RES	75	75	GAMMA-CARBOXYGLUTAMIC ACID (BY
FT	MOD_RES	79	79	GAMMA-CARBOXYGLUTAMIC ACID (BY

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FT MOD_RES 103 103 SIMILARITY).
FT ACT_SITE 274 274 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 320 320 CHARGE RELAY SYSTEM.
FT ACT_SITE 417 417 CHARGE RELAY SYSTEM.
FT DISULFID 90 101 BY SIMILARITY.
FT DISULFID 95 110 BY SIMILARITY.
FT DISULFID 112 121 BY SIMILARITY.
FT DISULFID 129 140 BY SIMILARITY.
FT DISULFID 136 149 BY SIMILARITY.
FT DISULFID 151 164 BY SIMILARITY.
FT DISULFID 172 340 INTERCHAIN (BY SIMILARITY).
FT DISULFID 239 244 BY SIMILARITY.
FT DISULFID 259 275 BY SIMILARITY.
FT DISULFID 388 402 BY SIMILARITY.
FT DISULFID 413 441 BY SIMILARITY.
FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 490 AA; 53965 MW; 3A39FA85AF2A6D11 CRC64;

Query Match 46.58; Score 93; DB 1; Length 490;
Best Local Similarity 38.6%; Pred. No. 4,76-08;
Matches 17; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

Oy 1 ANSFLXLRHGSIXKXICDFFXAKKIFONVDTLAFSKH 44
Db 41 ANSFLLELKGNLRECKMEKNSYEALVEDEKREKTFEWMKY 84

RESULT 11
ID FA7_BOVIN STANDARD: PRT: 407 AA.
AC P22457;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE COAGULATION FACTOR VII (EC 3.4.21.21) (SERUM PROTHROMBIN CONVERSION ACCELERATOR).
CN F7.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
OC NCBI_Taxid=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=89008362; PubMed=3049594;
RA Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T., Iwanaga S.;
RT "Bovine factor VII. Its purification and complete amino acid sequence."
RL J. Biol. Chem. 263:14868-14877(1988).
RN [2]
RP STRUCTURE OF CARBOHYDRATE ON SER-52.
RX MEDLINE=89213999; PubMed=3149637;
RA Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T., Miyata T., Iwanaga S., Takao T., Shimonishi Y., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in bovine blood coagulation factors VII and IX."
RL J. Biochem. 104:867-868(1988).
RN [3]
RP STRUCTURE OF CARBOHYDRATE ON SER-52.
RX MEDLINE=91344709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the first EGF-like domain of clotting factors VII and IX and protein Z."
RL Adv. Exp. Med. Biol. 281:121-131(1990).
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa

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CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
CC -1- CATALYTIC ACTIVITY: HYDROLYSES ONE ARG-1-ILE BOND IN FACTOR X TO FORM FACTOR Xa.
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PPM: THE VITAMIN K-DEPENDENT. ENZYMATIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
DR PIR: A31979; A31979.
DR MEROPS: S01.215. -.
DR InterPro: IPR000152; -.
DR InterPro: IPR000294; -.
DR InterPro: IPR000561; -.
DR InterPro: IPR001254; -.
DR InterPro: IPR001314; -.
DR InterPro: IPR001438; -.
DR InterPro: IPR001881; -.
DR InterPro: IPR002383; -.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PRO0001; GLABLOOD.
DR PRINTS: PRO0010; EGFIBLOOD.
DR PRINTS: PRO0722; CHYMOTRYPSIN.
DR PROSITE: PS00010; ASX_HYDROXYL. 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
KW Hydrolyase; Serine protease; Blood coagulation; zymogen; Glycoprotein; Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid; EGF-like domain; Repeat.
KW EGF-like domain; Repeat.
FT CHAIN 1 152 FACTOR VII LIGHT CHAIN.
FT CHAIN 153 407 FACTOR VII HEAVY CHAIN.
FT DOMAIN 6 35 EGF-RICH.
FT DOMAIN 46 82 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 87 128 EGF-LIKE 2.
FT DOMAIN 153 407 CATALYTIC.
FT SITE 152 153 CLEAVAGE (BY FACTOR Xa, FACTOR XIa, FACTOR IXa, OR THROMBIN).
FT ACT_SITE 193 193 BY SIMILARITY.
FT ACT_SITE 242 242 BY SIMILARITY.
FT ACT_SITE 344 344 BY SIMILARITY.
FT BINDING 338 338 SUBSTRATE (BY SIMILARITY).
FT DISULFID 17 22 BY SIMILARITY.
FT DISULFID 50 61 BY SIMILARITY.
FT DISULFID 55 70 BY SIMILARITY.
FT DISULFID 72 81 BY SIMILARITY.
FT DISULFID 91 102 BY SIMILARITY.
FT DISULFID 98 112 BY SIMILARITY.
FT DISULFID 114 127 BY SIMILARITY.
FT DISULFID 135 262 BY SIMILARITY.
FT DISULFID 159 164 BY SIMILARITY.
FT DISULFID 178 194 BY SIMILARITY.
FT DISULFID 310 329 BY SIMILARITY.
FT DISULFID 340 368 BY SIMILARITY.
FT MOD_RES 6 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 7 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 14 14 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 16 16 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 19 19 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 20 20 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 25 25 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 26 26 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 29 29 GAMMA-CARBOXYGLUTAMIC ACID.

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FT MOD_RES 35 35 GAMMA-CARBOXYGLUTAMIC ACID.
FT CARBOHYD 52 52 O-LINKED (GLC. . .).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .).
FT CARBOHYD 203 203 N-LINKED (GLCNAC. . .).
SO SEQUENCE 407 AA; 44431 MW; 703ELFE06367F10 CRC64;

Query Match 45.0%; Score 90; DB 1; Length 407;
Best Local Similarity 46.3%; Pred. No. 1,2e-07;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANSLXLYLRHSLXRCIXICDPYXAKXIFQNVDTLAFW 41
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 1 ANGFLLEILPGLERECREELCFEEAHEIFRNEERTKOFW 41

RESULT 12
THRB_RAT
ID THRB_RAT STANDARD; PRT; 617 AA.
AC P18292;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE PROTHROMBIN PRECURSOR (EC 3.4.21.5).
GN F2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RX MEDLINE=90332426; PubMed=2377469;
RA Dhanich M., Monard D.;
RT "cDNA sequence of rat prothrombin";
RN Nucleic Acids Res. 18:4251-4251(1990).
RN [2]
RP SEQUENCE OF 383-617 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92212913; PubMed=1557383;
RA Banfield D.K., Macgillivray R.T.;
RT "Partial characterization of vertebrate prothrombin cDNAs:
RT amplification and sequence analysis of the B chain of thrombin from
RT nine different species.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
CC -1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS
CC FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
CC AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.
CC -1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
CC RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL
CC ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
CC ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
CC OF PROTHROMBIN TO THROMBIN.
CC -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
CC PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
CC FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS. FACTOR XA REMOVES
CC THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
CC HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
CC V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
CC THROMBIN.
CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
CC FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
CC BY FACTOR XA.
CC -1- SIMILARITY: CONTAINS 2 KRINGLE REGIONS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC -----
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CC -----
DR EMBL; X52835; CA37017.1; -
DR EMBL; M81397; AAA42240.1; -
DR PIR; S10511; S10511.
DR HSSP; P00734; 10VS.
DR MEROPS; S01.217; -.
DR InterPro; IPR000001; -.
DR InterPro; IPR000294; -.
DR InterPro; IPR001254; -.
DR InterPro; IPR001314; -.
DR InterPro; IPR002383; -.
DR Pfam; PF00594; glg1.1.
DR Pfam; PF00051; kringle_2.
DR Pfam; PF00089; trypsin_1.
DR PRINTS; PR00001; GLABLOOD.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00021; KRINGLE_1; 2.
DR PROSITE; PS00134; TRYPSIN_HIS_1.
DR PROSITE; PS00135; TRYPSIN_SER_1.
DR PROSITE; PS50070; KRINGLE_2; 2.
KW Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Duplication;
KW Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver;
KW Hydrolyase; Serine protease; Kringle; Signal.
FT SIGNAL 1 ?
FT PROPEP 43 ?
FT CHAIN 44 617 PROTHROMBIN.
FT PEPTIDE 44 200 ACTIVATION PEPTIDE (FRAGMENT 1).
FT PEPTIDE 201 323 ACTIVATION PEPTIDE (FRAGMENT 2).
FT CHAIN 324 359 THROMBIN LIGHT CHAIN (A).
FT CHAIN 360 617 THROMBIN HEAVY CHAIN (B).
FT DOMAIN 109 187 KRINGLE 1.
FT DOMAIN 215 292 KRINGLE 2.
FT DOMAIN 360 617 CATALYTIC.
FT SITE 200 201 CLEAVAGE (BY THROMBIN).
FT SITE 323 324 CLEAVAGE (BY FACTOR XA).
FT SITE 359 360 CLEAVAGE (BY FACTOR XA).
FT ACT_SITE 402 402 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 458 458 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 564 564 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT MOD_RES 50 50 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 51 51 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 58 58 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 63 63 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 64 64 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 73 73 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 76 76 GAMMA-CARBOXYGLUTAMIC ACID.
FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 412 412 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 61 66 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 91 104 BY SIMILARITY.
FT DISULFID 109 187 BY SIMILARITY.
FT DISULFID 130 170 BY SIMILARITY.
FT DISULFID 158 182 BY SIMILARITY.
FT DISULFID 215 292 BY SIMILARITY.
FT DISULFID 236 276 BY SIMILARITY.
FT DISULFID 264 287 BY SIMILARITY.
FT DISULFID 332 478 INTERCHAIN (BY SIMILARITY).
FT DISULFID 387 403 BY SIMILARITY.
FT DISULFID 532 546 BY SIMILARITY.
FT DISULFID 560 590 BY SIMILARITY.
SO SEQUENCE 617 AA; 70411 MW; AD27D1B71445DB1D CRC64;

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Query Match

41.28;

Score 82.5; DB 1; Length 617;

DB 44 ANSGLEELRGNTERECVEBQCSYEAEFALESPODTVFWAKY 88

RESULT 14

PRIS_MACMU STANDARD: PRT: 649 AA.

AC Q28520; 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (FRAGMENT).

GN PROSI OR PROS.

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cebropithecoidea; Macaca.

OX NCBI_TaxID=9544;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA MEDLINE=95134217; PubMed=7832752;

RT "Identification of candidate residues for interaction of protein S with C4b binding protein and activated protein C.";

RL Biochem. J. 305:397-403(1995).

CC -1- FUNCTION: ANTICOAGULANT PLASMA PROTEIN; IT IS A COFACTOR TO ACTIVATED PROTEIN C IN THE DEGRADATION OF COAGULATION FACTORS VA AND VIIIA. IT HELP TO PREVENT COAGULATION AND STIMULATING FIBRINOLYSIS.

CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.

CC -1- TISSUE SPECIFICITY: PLASMA.

CC -1- SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.

CC -1- SIMILARITY: CONTAINS 4 EGF-LIKE DOMAINS.

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CC -----

DR EMBL: L31380; AAA70376.1; ALT_INT.

DR HSP: P00740; IGFH.

DR InterPro: IPR000152; -

DR InterPro: IPR000294; -

DR InterPro: IPR000561; -

DR InterPro: IPR001791; -

DR InterPro: IPR001881; -

DR Pfam: PF00008; EGF_4.

DR Pfam: PF00594; g1a; 1.

DR Pfam: PF00054; laminin_G; 1.

DR PROSITE: PS00010; ASX_HYDROXYL; 4.

DR PROSITE: PS00011; GLU CARBOXYLATION; 1.

DR PROSITE: PS00022; EGF_1; 1.

DR PROSITE: PS01186; EGF_2; 3.

DR PROSITE: PS01187; EGF_CA; 3.

KW Plasma; Gamma-carboxyglutamic acid; Calcium; Vitamin K; Zymogen;

KW Blood coagulation; Hydroxylation; Glycoprotein; Repeat;

KW EGF-like domain.

FT NON_FBR 1 1

FT PROPEP <1 14

FT CHAIN 15 649

FT DOMAIN 15 59

FT DOMAIN 60 89

FT DOMAIN 90 128

FT DOMAIN 130 173

FT DOMAIN 174 215

FT DOMAIN 216 236

FT MOD_RES 20 20

FT MOD_RES 21 21

FT MOD_RES 21 21

BY SIMILARITY.

VITAMIN K-DEPENDENT PROTEIN S.

GLA.

THROMBIN-SENSITIVE.

EGF-LIKE 1.

EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).

GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).

GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).

FT MOD_RES 28 28

FT MOD_RES 30 30

FT MOD_RES 33 33

FT MOD_RES 34 34

FT MOD_RES 39 39

FT MOD_RES 40 40

FT MOD_RES 43 43

FT MOD_RES 46 46

FT MOD_RES 50 50

FT MOD_RES 109 109

FT DISULFID 94 107

FT DISULFID 99 116

FT DISULFID 118 127

FT DISULFID 134 148

FT DISULFID 144 157

FT DISULFID 159 172

FT DISULFID 178 190

FT DISULFID 185 199

FT DISULFID 201 214

FT DISULFID 220 229

FT DISULFID 225 238

FT DISULFID 240 255

FT CARBOHYD 472 472

FT CARBOHYD 482 482

FT CARBOHYD 503 503

SO SEQUENCE 649 AA; 72402 MW; 5C7C13D31C7E96B CRC64;

Query Match 41.0%; Score 82; DB 1; Length 649;

Best Local Similarity 36.4%; Pred. No. 4.7e-06;

Matches 16; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGLKRCIXICDFXAKXIFQNDPLAFMSKH 44

DB 15 ANSMLEETKOGNLECELECNKEAREVFNDEPDTYEPKY 58

RESULT 15

PRIS_HUMAN STANDARD: PRT: 676 AA.

AC P07225; Q15518; 01-APR-1988 (Rel. 07, Created)

DT 01-APR-1988 (Rel. 07, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE VITAMIN K-DEPENDENT PROTEIN S PRECURSOR.

GN PROSI OR PROS.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91084444; PubMed=2148110;

RA Schmidt D.R., Tatro A.V., Phelps L.G., Tomczak J.A., Long G.L.;

RT "Organization of the human protein S genes.";

RL Biochemistry 29:7845-7852(1990).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Ploos van Amstel H.K.;

RL Submitted (AUG-1987) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE OF 27-676 FROM N.A.

RX MEDLINE=91084445; PubMed=2148111;

FT	DISULFID	161	175	BY SIMILARITY.
FT	DISULFID	171	184	BY SIMILARITY.
FT	DISULFID	186	199	BY SIMILARITY.
FT	DISULFID	205	217	BY SIMILARITY.
FT	DISULFID	212	226	BY SIMILARITY.
FT	DISULFID	228	241	BY SIMILARITY.
FT	DISULFID	247	256	BY SIMILARITY.
FT	DISULFID	252	265	BY SIMILARITY.
FT	DISULFID	267	282	BY SIMILARITY.
FT	CARBOHYD	499	499	N-LINKED (GLCNAC. . .); EXCEPT IN VARIANT HEERLEN.
FT	CARBOHYD	509	509	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	530	530	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARIANT	196	196	K -> E (IN TOKUSHIMA; PROS DEFICIENCY).
FT	VARIANT	258	258	/FTId=VAR_005566. N -> S (IN PROS DEFICIENCY).
FT	VARIANT	501	501	/FTId=VAR_005567. S -> P (IN HEERLEN).
FT	CONFLICT	11	11	/FTId=VAR_005568. L -> P (IN REF. 5).
FT	CONFLICT	26	26	F -> L (IN REF. 5).
SO	SEQUENCE	676 AA;	75122 MW;	2B88A04F85403F25 CRC64;

Query Match 41.08; Score 82; DB 1; Length 676;
 Best Local Similarity 36.4%; Pred. No. 4.9e-06;
 Matches 16; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

OY 1 ANSFLXXLRHGSIXXCIXXICDPXAXXIFQONVDDTLAFWSKH 44
 DB 42 ANSLLEETKQGNLEKCEIEELCNKEARAEVFNDEPDTYFPKY 85

Search completed: November 8, 2001, 08:56:10
 Job time: 174 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 8, 2001, 08:50:01 ; Search time 13.45 Seconds
(without alignments)
249.196 Million cell updates/sec

Title: US-09-497-591-1
Perfect score: 200
Sequence: 1 ANSFLXXLRHSGSLXRCIXX.....XXAKXLFQNVDTLAFMSKH 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	176	88.0	461	1 KXHU	protein C (activat
2	147	73.5	461	1 UX0210	protein C (activat
3	146	73.0	461	1 S18994	protein C (activat
4	129	64.5	456	1 KXBO	protein C (activat
5	105	52.5	482	1 EXRT	coagulation factor
6	104	52.0	443	2 I46932	coagulation factor
7	101	50.5	492	1 EXBO	coagulation factor
8	100	50.0	488	1 EXHU	coagulation factor
9	93	46.5	466	1 KFH07	coagulation factor
10	90	45.0	407	1 KFB07	coagulation factor
11	82.5	41.2	617	2 S10511	thrombin (EC 3.4.2
12	82.5	41.2	618	2 A35827	thrombin (EC 3.4.2
13	82	41.0	642	2 S53434	plasma protein S p
14	82	41.0	676	1 KXHUS	plasma protein S p
15	81	40.5	452	1 A30351	coagulation factor
16	81	40.5	459	2 J00419	coagulation factor
17	81	40.5	466	2 S38819	plasma protein S -
18	80	40.0	622	1 TBHU	thrombin (EC 3.4.2
19	80	40.0	675	1 KXBOS	plasma protein S p
20	78	39.0	675	1 KXRTS	plasma protein S p
21	77	38.5	461	1 KFHU	coagulation factor
22	77	37.5	642	1 S53433	plasma protein S p
23	74	37.0	416	1 KFB0	coagulation factor
24	73	36.5	475	1 EXCH	coagulation factor
25	71	35.5	675	1 KXMS	plasma protein S p
26	68	34.0	625	1 TBBO	thrombin (EC 3.4.2
27	65.5	32.8	422	1 KKHU2	plasma protein S p
28	62	31.0	673	2 A48089	growth arrest-spec
29	61	30.5	674	2 I55476	growth potentialin

30	60	30.0	678	2 B48089	growth arrest-spec
31	59.5	29.8	396	1 KXB02	plasma protein 2 -
32	51.5	25.8	594	2 D84859	probable MAP kinase
33	51	25.5	245	2 S49045	luxp protein - Vib
34	49.5	24.8	510	2 E82918	ammonium transport
35	49.5	24.8	603	2 C96575	probable MAP kinase
36	49	24.5	422	2 T39306	mitogen-activated
37	49	24.5	730	2 G64062	primosomal replica
38	48	24.0	605	2 T40556	hypothetical prote
39	47.5	23.8	489	2 S69027	ammonium transport
40	47.5	23.8	576	2 G96763	probable MAP kinase
41	47	23.5	390	2 T14794	hypothetical prote
42	47	23.5	467	2 S36559	l2 protein - human
43	47	23.5	628	2 T04252	probable phosphati
44	47	23.5	1330	2 S49010	embryonic receptor
45	47	23.5	1333	2 I78875	receptor tyrosine

ALIGNMENTS

RESULT 1

KXHU

protein C (activated) (EC 3.4.21.69) precursor - human
N:Alternate names: autoprothrombin IIA; plasma protein C
C:Species: Homo sapiens (man)

C>Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
C:Accession: A22331; A25426; A21781; A23789; A00927

R:Foster, D.C.; Yoshitake, S.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985

A>Title: The nucleotide sequence of the gene for human protein C.
A:Reference number: A22331; MUID:85270390

A:Accession: A22331

A:Molecule type: DNA

A:Residues: 1-461 <FOS1>

A:Cross-references: GB:M1228; NID:g190333; PIDN:AAA60166.1; PID:g190334
R:Plutsky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.
Proc. Natl. Acad. Sci. U.S.A. 83, 5465-550, 1986

A>Title: Evolution and organization of the human protein C gene.
A:Reference number: A25426; MUID:86120978

A:Accession: A25426

A:Molecule type: DNA

A:Residues: 1-445, 'L', '446-461 <PDU>

A:Cross-references: GB:M12712; NID:g190330; PIDN:AAA60165.1; PID:g190332
R:Foster, D.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984

A>Title: Characterization of a cDNA coding for human protein C.
A:Reference number: A21781; MUID:84272714

A:Accession: A21781

A:Molecule type: mRNA

A:Residues: 'Q', 107-461 <FOS2>

A:Cross-references: GB:K02058; NID:g190322; PIDN:AAA60164.1; PID:g190323
R:Beckmann, R.J.; Schmidt, R.J.; Santner, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G.
Nucleic Acids Res. 13, 5233-5247, 1985

A>Title: The structure and evolution of a 461 amino acid human protein C precursor an
A:Reference number: A23789; MUID:85269639

A:Accession: A23789

A:Molecule type: mRNA

A:Residues: 1-461 <BEC>

A:Cross-references: GB:X02750; NID:g35689; PIDN:CAA26528.1; PID:g763120
R:Milietich, J.P.; Broze Jr., G.J.
J. Biol. Chem. 265, 11397-11404, 1990

A>Title: Beta protein C is not glycosylated at asparagine 329. The rate of translatio
A:Contents: annotation; carbohydrate binding sites; activation peptide
A>Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is

R:Harris, R.J.; Ling, V.T.; Spellman, M.W.
J. Biol. Chem. 267, 5102-5107, 1992
A>Title: O-linked fucose is present in the first epidermal growth factor domain of fa
A:Contents: annotation; beta-hydroxyaspartic acid
A:Comment: protein C is the zymogen of the vitamin K-dependent serine proteinase that
ivation of factor Va is strongly enhanced by complexing with protein S. Protein C als

C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is
bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction,
C:Genetics:
A:Gene: GDB:PROC
A:Cross-references: GDB:120317; OMIM:176860
A:Map position: 2q13-q21
A:Introns: 24/1; 79/3; 86/1; 134/1; 179/1; 226/3; 266/1
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: anticoagulant; beta-hydroxyaspartic acid; Gla domain homology; calcium binding
F:1-32/Domain: signal sequence #status predicted <SIG>
F:12-86/Domain: Gla domain homology <Gla>
F:33-42/Domain: propeptide #status predicted <PRO>
F:43-197/Product: protein C light chain #status predicted <LCH>
F:92-131/Domain: EGF homology <EG1>
F:140-175/Domain: EGF homology <EG2>
F:200-461/Product: protein C heavy chain #status predicted <CH>
F:200-211/Domain: activation peptide #status experimental <AP>
F:212-445/Domain: trypsin homology <TRY>
F:48-49,56,58,61,62,67,68,71/Modified site: gamma-carboxyglutamic acid (Glu) #status exp
F:59-64,92-105,101-120,122-131,140-151,147-160,162-175,183-199,238-254,373-387,398-426/D
F:106-111/Disulfide bonds: #status predicted
F:110/Binding site: carbohydrate (Thr) (covalent) #status absent
F:113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:139,220,355/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:211-212/Cleavage site: Arg-Leu (thrombin) #status experimental
F:253,299,400/Active site: His, Asp, Ser #status predicted
F:371/Binding site: carbohydrate (Asn) (covalent) (partial) #status atypical

Query Match 88.0% Score 176: DR 1: Length 461:
Best Local Similarity 77.3% Pred. No. 5e-21;
Matches 34: Conservative 0: Mismatches 10: Indels 0: Gaps 0:

OY 1 ANSFPLRHSGSLRXRCIXICDFFXKXKIFQNVDDTLAFWSKH 44
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 43 ANSFLRELHSHSLERECIEICDFEAKETIFQVNDTLAFPSKH 86

RESULT 2
JX0210
protein C (activated) (EC 3.4.21.69) precursor - mouse
N:Alternate names: vitamin K-dependent serine proteinase
C:Species: Mus musculus (house mouse)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: JX0210
R:Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.
J. Biochem. 111, 491-495, 1992
A:Title: Isolation and characterization of a mouse protein C cDNA.
A:Reference number: JX0210; MUID:92316897
A:Accession: JX0210
A:Molecule type: mRNA
A:Residues: 1-461 <TAD>
A:Cross-references: GB:D10445; NID:g220385; PIDN:BAA01235.1; PID:g220386
A:Experimental source: liver
S:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re-

S:
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
F:1-33/Domain: signal sequence #status predicted <SIG>
F:27-85/Domain: Gla domain homology <Gla>
F:34-41/Domain: propeptide #status predicted <PRO>
F:42-196,199-461/Product: protein C #status predicted <PRC>
F:42-196/Domain: light chain #status predicted <PCL>
F:91-130/Domain: EGF homology <EG1>
F:139-174/Domain: EGF homology <EG2>
F:199-461/Domain: heavy chain #status predicted <PCH>
F:199-211/Domain: activation peptide #status experimental <ACT>
F:212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIT>
F:212-445/Domain: trypsin homology <TRY>
F:47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status
F:112-130,139-150,146-159,161-174,182-319,238-254,373-387,398-426/Disulfide bonds: #stat
F:214,230,355/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

F:253,299,402/Active site: His, Asp, Ser #status predicted

Query Match          73.5%;   Score 147;   DB 1;   Length 461;
Best Local Similarity 63.6%;   Pred. No. 3e-16;
Matches 28; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

OY      1 ANSFLXLRHGSLXRXCJXXICDFFXAXKXIFQNVDTLAFWSKH 44
        ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
DB      42 ANSFLEEMRPGSLERECMEBETCDFEEDAEITFQNVDTLAFWIKY 85

RESULT 3
protein C (activated) (EC 3.4.21.69) precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text-change 29-Oct-1999
C:Accession: S18994; S24312
R:Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
submitted to the EMBL Data Library, February 1992
A:Description: The cDNA cloning and mRNA expression of rat protein C.
A:Reference number: S18994
A:Accession: S18994
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-461 <OK>
A:Cross-references: EMBL:X64336; NID:g56962; PINN:CAA45617.1; PID:g56963
R:Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
Biochim. Biophys. Acta 1131, 329-332, 1992
A>Title: The cDNA cloning and mRNA expression of rat protein C.
A:Reference number: S24312; MUID:92329550
A:Accession: S24312
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-461 <OKA2>
A:Cross-references: EMBL:X64336; NID:g56962; PINN:CAA45617.1; PID:g56963
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homolog
C:Keywords: beta-hydroxyaspartic acid; glycoprotein; hydrolase; serine proteinase
F:1-32/Domain: signal sequence #status predicted <SIG>
F:1-7-85/Domain: Gla domain homology <GLA>
F:33-42/Domain: propeptide #status predicted <PRO>
F:43-461/Product: protein C #status predicted <PRC>
F:91-130/Domain: EGF homology <EG1>
F:139-174/Domain: EGF homology <EG2>
F:213-445/Domain: trypsin homology <TRY>
F:47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #stat
F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:121-130,139-150,146-159,161-174,182-320,239-255,273-387,398-426/Disulfide bonds: #s
F:254,300,402/Active site: His, Asp, Ser #status predicted

Query Match          73.0%;   Score 146;   DB 1;   Length 461;
Best Local Similarity 63.6%;   Pred. No. 4.3e-16;
Matches 28; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

OY      1 ANSFLXLRHGSLXRXCJXXICDFFXAXKXIFQNVDTLAFWSKH 44
        ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
DB      42 ANSFLEEVRAAGSLERECMEBETCDFEEDAEITFQNVDTLAFWIKY 85

RESULT 4
KXBO
protein C (activated) (EC 3.4.21.69) precursor - bovine (fragment)
N:Alternate names: autoproteohombin IIA; plasma protein C
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Nov-1980 #sequence revision 17-Mar-1987 #text-change 16-Jul-1999
C:Accession: A26250; A18385; A18386; A00928
R:Piong, G.L.; Balagaje, R.M.; Macgillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 81, 5653-5656, 1984
A>Title: Cloning and sequence of liver cDNA coding for bovine protein C.
A:Reference number: A26250; MUID:85014826

```

A:Molecule type: mRNA
A:Residues: 1-456 <LON>
R:Fernlund, P.; Stenflo, J.
J. Biol. Chem. 257, 12170-12179, 1982
A:Title: Amino acid sequence of the light chain of bovine protein C.
A:Reference number: A18385; MUID:83007325
A:Accession: A18385
A:Molecule type: protein
A:Residues: 40-194 <FER>
A:Note: 82-Lys was also found
R:Driksenberg, T.; Fernlund, P.; Roepstorff, P.; Stenflo, J.
Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983
A:Title: beta-hydroxyaspartic acid in vitamin K-dependent protein C.
A:Reference number: A19316; MUID:83169769
A:Contents: annotation; revision to residue 110
R:Stenflo, J.; Fernlund, P.
J. Biol. Chem. 257, 12180-12190, 1982
A:Title: Amino acid sequence of the heavy chain of bovine protein C.
A:Reference number: A18386; MUID:83007326
A:Accession: A18386
A:Molecule type: protein
A:Residues: 197-454, 'PV' <STF>
R:Esmon, N.L.; Debault, L.E.; Esmon, C.T.
J. Biol. Chem. 258, 5548-5553, 1983
A:Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless F
A:Reference number: A37541; MUID:83213513
A:Contents: annotation; activation; calcium binding
R:Johnson, A.E.; Esmon, N.L.; Laue, T.M.; Esmon, C.T.
J. Biol. Chem. 258, 5554-5560, 1983
A:Title: Structural changes required for activation of protein C are induced by Ca2+ bin
A:Reference number: A37542; MUID:83213514
A:Contents: annotation; activation; calcium binding
C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re
B:
C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is d
bin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this react
C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strc
cognition of the thrombin-thrombomodulin complex.
C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding
F:1-29/Domain: signal sequence (fragment) #status predicted <SIG>
F:30-39/Domain: Gla domain homology <Gla>
F:40-194/Product: propeptide #status predicted <PRO>
F:98-128/Domain: EGF homology <EG1>
F:137-112/Domain: EGF homology <EG2>
F:197-456/Product: protein C heavy chain #status experimental <HCH>
F:197-210/Domain: activation peptide #status experimental <APF>
F:211-440/Domain: trypsin homology <TRY>
F:45, 46, 53, 55, 58, 59, 62, 64, 65, 68, 74/Modified site: gamma-carboxyglutamic acid (Glu) #stat
F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:119-128, 137-148, 144-157, 159-172, 180-318, 237-253, 368-382, 393-421/Dsulfide bonds: #stat
F:136, 288, 350/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:252, 298, 397/Active site: His, Asp, Ser #status predicted
F:366/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 64.5%; Score 129; DB 1; Length 456;
Best Local Similarity 54.8%; Pred. No. 2.7e-13;
Matches 23; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANSFLXLRHGSILRXRCIXXICDFXXAKXIFONVDTLAFWS 42
DB 40 ANSFLELRPGNVERCESECEFEAREIFONTDTAFWS 81

RESULT 5
EXRT
coagulation factor Xa (EC 3.4.21.6) precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Jan-1995 #sequence_revision 07-Feb-1997 #text_change 08-Dec-2000
C:Accession: S49075; J04670; PS0191; PS0190; I62745

R:Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
Thromb. Res. 80, 63-73, 1995
A:Title: Evidence for competition between vitamin K-dependent clotting factors for in
A:Reference number: A58498; MUID:96093366
A:Accession: S49075
A:Molecule type: mRNA
A:Residues: 1-482 <STAL>
A:Cross-references: EMBL:X79807; NID:9506600; PIDN:CA56202.1; PID:9506601
A:Note: submitted to the EMBL Data Library, June 1994
A:Note: neither the complete nucleic acid sequence nor the complete translation are s
R:Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
Gene 169, 269-273, 1996
A:Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.
A:Reference number: J04670; MUID:96194815
A:Accession: J04670
A:Molecule type: mRNA
A:Residues: 1-482 <STAL>
A:Cross-references: EMBL:X79807; NID:9506600; PIDN:CA56202.1; PID:9506601
A:Experimental source: Cos-1 cell
R:Enjoli, K.; Miyazaki, K.; Kato, H.
J. Biochem. 109, 890-898, 1991
A:Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat
A:Reference number: PS0190; MUID:92041742
A:Accession: PS0191
A:Molecule type: protein
A:Residues: 41-58, 'X', 60-65 <ENJ>
A:Accession: PS0190
A:Molecule type: protein
A:Residues: 183-186, 'X', 188-207 <ENJ2>
R:Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.
Eur. J. Haematol. 52, 162-168, 1994
A:Title: Analysis of the partial nucleotide sequences and deduced primary structures
A:Reference number: I46196; MUID:94222160
A:Accession: I62745
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 295-383, 'G', 385-455 <MUR>
A:Cross-references: GB:D21215; NID:9415309; PIDN:BAA04756.1; PID:9455396
C:Function:
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the
A:Pathway: blood coagulation
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-40/Domain: propeptide #status predicted <PRO>
F:25-84/Domain: Gla domain homology <Gla>
F:41-179/Product: coagulation factor X light chain #status predicted <LCH>
F:90-121/Domain: EGF homology <EG1>
F:129-164/Domain: EGF homology <EG2>
F:183-482/Product: coagulation factor X heavy chain #status predicted <HCH>
F:183-231/Domain: activation peptide #status predicted <APF>
F:232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>
F:233-460/Domain: trypsin homology <TRY>
F:46, 47, 54, 56, 59, 60, 65, 66, 69, 72, 79/Modified site: gamma-carboxyglutamic acid (Glu) #s
F:57-62, 90-101, 95-110, 112-121, 129-149, 136-149, 151-164, 172-340, 238-243, 259-275, 388-402
F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:187/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:208/Binding site: carbohydrate (Thr) (covalent) #status predicted
F:218/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:231-232/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #s
F:274, 320, 417/Active site: His, Asp, Ser #status predicted

Query Match 52.5%; Score 105; DB 1; Length 482;
Best Local Similarity 38.6%; Pred. No. 2.6e-09;
Matches 17; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANSFLXLRHGSILRXRCIXXICDFXXAKXIFONVDTLAFWSKH 44
DB 41 ANSFLELRKGNLRECEVCETCSFEAREVPEDNKRTTFWPKY 84

RESULT 6

A.Residues: 1-466 <GAB>
A.Cross-references: GB:M13232; NID:g182799; PIDN:AAA8040.L; PID:g182801
R.Thim, L.; Bjørn, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.
Biochimica 27, 7785-7793, 1988
A.Title: Amino acid sequence and posttranslational modifications of human factor VII-a f
A.Reference number: A90539; MUID:89088153
A.Accession: A31186
A.Molecule type: protein
A.Residues: 61-212 <THI>
A.Accession: B31186
A.Molecule type: protein
A.Residues: 213-466 <H2>
R.Björn, S.; Foster, D.C.; Thim, L.; Wberg, F.C.; Christensen, M.; Komiyama, Y.; Peder
J. Biol. Chem. 266, 11051-11057, 1991
A.Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations a
A.Reference number: A40529; MUID:91250411
A.Contents: annotation; carbohydrate binding sites
Eur. J. Biochem. 234, 293-300, 1995
A>Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carbox
A.Reference number: S63524; MUID:96096752
A.Accession: S63524
A.Molecule type: protein
A.Residues: 61-65; 99-103; 105-109; 213-217; 308-312 <PER>
C.Genes:
A.Gene: GDB:F7
A.Cross-references: GDB:119897; OMIM:227500
A.Map position: 13q34-13q34
A.Introns: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1
C.Function:
A.Description: catalyzes the proteolytic activation of coagulation factor X in the presen
ogulation factor IX in the presence of calcium and tissue factor
A.Pathway: blood coagulation extrinsic pathway
C.Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C.Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutami
F.1-20/Domain: signal sequence #status predicted <SIG>
F.21-60/Domain: propeptide #status predicted <PRO>
F.45-104/Domain: Gla domain homology <GLA>
F.61-212/Product: coagulation factor VIIa light chain #status experimental <MA1>
F.110-141/Domain: EGF homology <EG1>
F.151-187/Domain: EGF homology <EG2>
F.213-466/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
F.213-447/Domain: trypsin homology <TRY>
F.66; 67; 74; 76; 79; 80; 85; 86; 89; 95/Modified site: gamma-carboxyglutamic acid (Glu) #status
F.77-82; 110-121; 115-130; 132-141; 151-162; 158-172; 174-187; 195-322; 219-224; 238-254; 370-389,
F.112; 120/Binding site: carboxhydrate (Ser) (covalent) #status experimental
F.123/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status absent
F.205; 382/Binding site: carboxhydrate (Asn) (covalent) #status experimental
F.212-213/Cleavage site: Arg-Ile (coagulation factor XIla) #status experimental
F.253; 302; 404/Active site: His, Asp, Ser #status predicted
F.350-351/Cleavage site: Arg-Gly (Coagulation factor Xa) #status predicted

Query Match 46.5%; Score 93; DB 1; Length 466;
Best Local Similarity 46.3%; Pred. No. 2,46-07;
Matches 19; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

OY 1 ANSEFLRLRHSLKXKCIXICDFYXAKXIFQNDDTIAFW 41
||| || | || | | | | : || : | |
Db 61 ANAFLELRPSGLERECKEEOCSFEAREIRFKDAERTLFW 101

RESULT 10
KFB07
coagulation factor VIIa (EC 3.4.21.21) - bovine
C.Species: Bos primigenius taurus (cattle)
C.Date: 21-May-1990 #sequence.revision 23-Mar-1995 #text.change 16-Jul-1999
C.Accession: A31979; C20274
R.Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.
J. Biol. Chem. 263, 14868-14877, 1988
A>Title: Bovine factor VII. Its purification and complete amino acid sequence.
A.Reference number: A31979; MUID:89008362
A.Accession: A31979

A:Molecule type: protein
A:Residues: 1-407 <TAK>
R:McMullen, B.A.; Fujikawa, K.; Kissel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1993
A>Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood
A:Reference number: A20274; MUID:83308813
A:Accession: C20274
A:Molecule type: protein
A:Residues: 58-62, 'X', 64-68 <MCW>
A>Note: The residue designated 'X' was determined to be hydroxyaspartic acid
R:Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga
J. Biochem. 104, 867-868, 1988
A>Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood c
A:Reference number: A44556; MUID:89213999
A:Contents: annotation
A>Note: structure and location of covalently bound carbohydrate
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the pr
gulation factor IX in the presence of calcium and tissue factor
A:Pathway: Blood coagulation extrinsic pathway
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamic
F:1-152/Product: coagulation factor VIIa light chain #status experimental <MA>
F:1-44/Domain: Gla domain homology (fragment) <GLA>
F:50-81/Domain: EGF homology <EG1>
F:91-127/Domain: EGF homology <EG2>
F:153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
F:153-387/Domain: trypsin homology <TRY>
F:167-14,16,19,20,25,26,29,34,35/Modified site: gamma-carboxylglutamic acid (Glu) #sta
F:17-22,50-61,55-70,72-81,91-102,98-112,114-127,135-262,159-164,178-194,310-329,340-3-3
F:52/Binding site: carbonyl (Ser) (covalent) #status experimental
F:63/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experim
F:145,203/Binding site: carboxylate (Asn) (covalent) #status experimental
F:153-153/Cleavage site: Arg-Ile (coagulation factor XIIIa) #status experimental
F:193,242,344/Active site: His, Asp, Ser #status predicted
F:290-291/Cleavage site: Arg-Gly (coagulation factor XIa) #status experimental

Query Match 45.0%; Score 90; DB 1; Length 407;
Best Local Similarity 46.3%; Pred. NO. 6,46-07;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANSFLRLRHGSIXRCIXICDFFXXARKIRONVDLAFW 41
DB 1 ANGFLLELLPGSLERECEBELCSFEFAHFRNERTKQFW 41

RESULT 11
SI0511
thrombin (EC 3.4.21.5) B chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 22-Jun-1999
C:Accession: SI0511; A60576; B42696
R:Dhanich, M.; Monard, D.
Nucleic Acids Res. 18, 4251, 1990
A>Title: cDNA sequence of rat prothrombin.
A:Reference number: SI0511; MUID:90332426
A:Accession: SI0511
A:Molecule type: mRNA
A:Residues: 1-617 <DH>
A:Cross-references: EMBL:X52835; NID:956969; PIDN:CA437017.1; PID:956970
R:Henrikson, K.P.; Jain, E.E.; Greenwood, J.A.; Dickerman, H.W.
Endocrinology 126, 167-175, 1990
A>Title: Prothrombin levels are increased in the estrogen-treated immature rat uterus
A:Reference number: A60576; MUID:90091942
A:Accession: A60576
A:Molecule type: protein
A:Residues: 44-58 <HEN>
A>Note: The authors purified the proenzyme from the estrogen-stimulated maturing rat
R:Barnfield, D.K.; MacCullivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A>Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and

A:Accession: B42696
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 383-617, 'E' <BAN>
A:Cross-references: GB:M81397
C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C:Keywords: blood coagulation; calcium binding; carboxylglutamic acid; glycoprotein; hydrolysis
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-43/Domain: propeptide #status predicted <PRO>
F:28-88/Domain: Gla domain homology <GLA>
F:44-617/Product: prothrombin #status experimental <PMAT>
F:109-187/Domain: kringle homology <KR1>
F:215-292/Domain: kringle homology <KR2>
F:360-609/Domain: trypsin homology <TRY>
F:501-51, 58, 60, 63, 64, 69, 70, 73, 76/Modified site: gamma-carboxylglutamic acid (Glu) #status
F:61-66, 91-104, 109-187, 130-170, 158-182, 215-292, 336-276, 264-287, 332-478, 387-403, 532-546, 5
F:402, 458, 564/Active site: His, Asp, Ser #status predicted

Query Match 41.2%; Score 82.5; DB 2; Length 617;
Best Local Similarity 40.0%; Pred. No. 1.7e-05;
Matches 18; Conservative 7; Mismatches 19; Indels 1; Gaps 1;

Oy 1 ANSFLXLRHGSIXKXICIXICDFFXAKXIFQNVDTLAFWSKH 44
Db 44 ANSGLEELRKGNLERECVECCSYEAFEALESPODIDVFWAKY 88

RESULT 12

thrombin (EC 3.4.21.5) B chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 14-Dec-1990 #sequence revision 14-Dec-1990 #text change 22-Jun-1999
C:Accession: A35827; A42696; S12081
R:Deben, S.J.F.; Schaefer, L.A.; Jamison, C.S.; Grant, S.G.; Fitzgibbon, J.J.; Pal, J.A.
DNA Cell Biol. 9, 487-498, 1990
A:Title: Characterization of the cDNA coding for mouse prothrombin and localization of the
A:Reference number: A35827; MUID:91025551
A:Accession: A35827
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-618 <DEC>
A:Cross-references: GB:M52308; NID:953813; PIDN:CAA36548.1; PID:953814
A:Experimental source: strain C57BL/6
A:Note: the data were obtained from females resulting from the cross of M. domesticus and
R:Banfield, D.K.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq
A:Reference number: A42696; MUID:92212913
A:Accession: A42696
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 384-618, 'E' <BAN>
A:Cross-references: GB:M81394
C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C:Keywords: blood coagulation; calcium binding; carboxylglutamic acid; glycoprotein; hydrolysis
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-43/Domain: propeptide #status predicted <PRO>
F:28-88/Domain: Gla domain homology <GLA>
F:44-617/Product: prothrombin B #status predicted <MAT>
F:109-187/Domain: kringle homology <KR1>
F:215-293/Domain: kringle homology <KR2>
F:361-610/Domain: trypsin homology <TRY>
F:501-51, 58, 60, 63, 64, 69, 70, 73, 76/Modified site: gamma-carboxylglutamic acid (Glu) #status
F:61-66, 91-104, 109-187, 130-170, 158-182, 215-292, 336-276, 264-288, 333-479, 388-404, 533-547, 5
F:403, 459, 565/Active site: His, Asp, Ser #status predicted

Query Match 41.2%; Score 82.5; DB 2; Length 618;
Best Local Similarity 40.0%; Pred. No. 1.7e-05;
Matches 18; Conservative 7; Mismatches 19; Indels 1; Gaps 1;

Oy 1 ANSFLXLRHGSIXKXICIXICDFFXAKXIFQNVDTLAFWSKH 44

Db 44 ANSGLEELRKGNLERECVECCSYEAFEALESPODIDVFWAKY 88

RESULT 13

plasma protein S precursor, vitamin K dependent - rhesus macaque (fragment)
C:Species: Macaca mulatta (rhesus macaque)
C:Date: 19-Mar-1997 #sequence revision 18-Jul-1997 #text change 16-Jul-1999
C:Accession: S53434
R:Greengard, J.S.; Fernandez, J.A.; Radtke, K.P.; Griffin, J.H.
Biochem. J. 305, 397-403, 1995
A:Title: Identification of candidate residues for interaction of protein S with C4b
A:Reference number: S53434; MUID:95132417
A:Accession: S53434
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-642 <GRE>
A:Cross-references: EMBL:L31380
A:Experimental source: tissue type liver
A:Note: the source is designated as rhesus monkey
C:Genetics:
A:Gene: PROS
C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat
F:1-51/Domain: Gla domain homology (fragment) <GLA>
F:1-7/Domain: signal sequence (fragment) #status predicted <SIG>
F:8-642/Product: plasma protein S #status predicted <MAT>
F:87-120/Domain: EGF homology <EG1>
F:127-165/Domain: EGF homology <EG2>
F:171-207/Domain: EGF homology <EG3>
F:213-248/Domain: EGF homology <EG4>
F:281-653/Domain: sex hormone-binding globulin homology <SHB>
F:291-444/Domain: laminin G repeat homology <LGR>

Query Match 41.0%; Score 82; DB 2; Length 642;
Best Local Similarity 36.4%; Pred. No. 2.1e-05;
Matches 16; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

Oy 1 ANSFLXLRHGSIXKXICIXICDFFXAKXIFQNVDTLAFWSKH 44
Db 8 ANSMLEETKQGNLERECIEELCKEAREVENDPDTFYPPKY 51

RESULT 14

plasma protein S precursor - human
C:Species: Homo sapiens (man)
C:Alternate names: vitamin K-dependent protein S
C:Date: 21-Sep-1990 #sequence revision 26-Jan-1996 #text change 16-Jul-1999
C:Accession: A35610; A35611; A26157; A25891; A36124; S02424; S09519
R:Schmidel, D.K.; Tatro, A.V.; Phelps, L.G.; Tomczak, J.A.; Long, G.L.
Biochemistry 29, 7845-7852, 1990
A:Title: Organization of the human protein S genes.
A:Reference number: A35610; MUID:91084444
A:Accession: A35610
A:Molecule type: DNA
A:Residues: 1-676 <SCH>
A:Cross-references: GB:M57853; NID:9190547; PIDN:AAA60357.1; PID:9190549; GB:J02917
A:Note: the authors translated the codon TTT for residue 26 as Leu
R:Ploos van Amstel, H.K.; Reitsma, P.H.; van der Logt, C.P.E.; Berltina, R.M.
Biochemistry 29, 7853-7861, 1990
A:Title: Intron-exon organization of the active human protein S gene Psalpa and its
A:Reference number: A35611; MUID:91084445
A:Accession: A35611
A:Molecule type: DNA
A:Residues: 1-25 <PL3>
A:Cross-references: GB:J02918
R:Hoskins, J.; Norman, D.K.; Beckmann, R.J.; Long, G.L.
Proc. Natl. Acad. Sci. U.S.A. 84, 349-353, 1987
A:Title: Cloning and characterization of human liver cDNA encoding a protein S precursor
A:Reference number: A26157; MUID:87092407
A:Accession: A26157

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OM protein - protein search, using sw model

Run on: November 8, 2001, 08:50:31 ; Search time 12.45 Seconds
(without alignments)
79.530 Million cell updates/sec

Title: US-09-497-591-1

Perfect score: 200
Sequence: 1 ANSFLXXLRHGSLSXRCIXX.....XXAKXIFQNVDDTLAFWSKH 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA: *
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/PC1US.COMB.pep: *
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	176	88.0	44	3	US-08-955-636-1
2	176	88.0	45	2	US-08-965-832-2
3	176	88.0	419	1	US-08-295-411-1
4	176	88.0	419	2	US-08-955-471-1
5	176	88.0	419	5	PCT-US92-10242-1
6	176	88.0	460	2	US-08-756-506-2
7	176	88.0	460	2	US-08-756-506-4
8	176	88.0	460	6	5270178-13
9	176	88.0	460	6	5270178-14
10	176	88.0	460	6	5270178-15
11	176	88.0	460	6	5270178-16
12	176	88.0	461	6	525557-2
13	176	88.0	461	6	5270178-17
14	176	88.0	461	6	5270178-18
15	176	88.0	461	6	5460953-3
16	168	84.0	44	3	US-08-955-636-19
17	168	84.0	44	3	US-08-955-636-24
18	166	83.0	44	3	US-08-955-636-35
19	163	81.5	42	2	US-08-745-254A-2
20	163	81.5	461	6	5270178-2
21	160	80.0	44	3	US-08-955-636-20
22	160	80.0	44	3	US-08-955-636-21
23	160	80.0	44	3	US-08-955-636-25
24	159	79.5	41	1	US-08-229-280-5
25	159	79.5	44	3	US-08-955-636-22
26	145	72.5	410	4	US-09-065-872-1
27	137	68.5	409	4	US-09-065-872-2

28	133	66.5	44	3	US-08-955-636-23	Sequence 23, Appl
29	123	61.5	44	3	US-08-955-636-2	Sequence 2, Appl
30	107	53.5	139	1	US-08-330-978-2	Sequence 2, Appl
31	107	53.5	139	1	US-08-474-042-2	Sequence 2, Appl
32	107	53.5	139	1	US-08-484-558-2	Sequence 2, Appl
33	107	53.5	139	1	US-08-774-592-2	Sequence 2, Appl
34	107	53.5	437	1	US-08-487-037-2	Sequence 2, Appl
35	107	53.5	437	1	US-08-487-037-3	Sequence 3, Appl
36	107	53.5	488	1	US-08-487-037-1	Sequence 1, Appl
37	101	50.5	487	1	US-08-469-486-53	Sequence 53, Appl
38	101	50.5	487	2	US-08-469-658-53	Sequence 53, Appl
39	101	50.5	492	1	US-08-469-486-2	Sequence 2, Appl
40	101	50.5	492	2	US-08-469-658-2	Sequence 2, Appl
41	100	50.0	448	1	US-08-295-411-3	Sequence 3, Appl
42	100	50.0	448	2	US-08-955-471-3	Sequence 3, Appl
43	100	50.0	448	5	PCT-US92-10068-1	Sequence 1, Appl
44	100	50.0	448	5	PCT-US92-10242-3	Sequence 3, Appl
45	96	48.0	44	3	US-08-955-636-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-955-636-1
Sequence 1, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE OF INVENTION: POLYPEPTIDES
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-1

Query Match 88.0%; Score 176; DB 3; Length 44;
Best Local Similarity 97.7%; Pred. No. 7.5e-23;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSLSXRCIXXIDFXXAKXIFQNVDDTLAFWSKH 44
Db 1 ANSFLXXLRHGSLSXRCIXXIDFXXAKXIFQNVDDTLAFWSKH 44

RESULT 2
US-08-965-832-2
Sequence 2, Application US/08965832
Patent No. 5847085
GENERAL INFORMATION:
APPLICANT: CHARLES T. ESMON AND MIKHAIL D. SMIRNOV
TITLE OF INVENTION: Modified Protein C
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 West
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:

```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,832
FILING DATE: 7-NOV-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/745,254
FILING DATE: 8-NOV-1996
PRIOR APPLICATION DATA: 60/053,768
FILING DATE: 25-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patricia L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMR# 165/167
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
OTHER INFORMATION: /note= "partial sequence of human protein C"
US-08-965-832-2

Query Match      88.0%; Score 176; DB 2; Length 45;
Best Local Similarity 97.7%; Pred. No. 7.7e-23;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSEFLXXLRH9SLXRXCIXXICDFXAKXIFQNVDDTLAFWSKH 44
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ANSEFLXXLRHSSLXRXCIXXICDFXAKXIFQNVDDTLAFWSKH 44

RESULT 3
US-08-295-411-1
; Sequence 1, Application US/08295411
; Patent No. 5679639
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Westers, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
```

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,411
FILING DATE: 22-AUG-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI263.0C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..157
OTHER INFORMATION: /note= "Protein C Light Chain"
NAME/KEY: Region
LOCATION: 158..169
OTHER INFORMATION: /note= "Protein C Activation"
OTHER INFORMATION: Peptide"
FEATURE:
NAME/KEY: Region
LOCATION: 170..419
OTHER INFORMATION: /note= "Protein C Heavy Chain"
US-08-295-411-1

Query Match      88.0%; Score 176; DB 1; Length 419;
Best Local Similarity 77.3%; Pred. No. 9.3e-22;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANSEFLXXLRH9SLXRXCIXXICDFXAKXIFQNVDDTLAFWSKH 44
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ANSEFLXELRHSSLXRXCIXXICDFEAKXIFQNVDDTLAFWSKH 44

RESULT 4
US-08-955-471-1
; Sequence 1, Application US/08955471
; Patent No. 5968751
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Westers, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
```


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PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
PT acid domain, useful for treating clotting disorders
XX
PS Disclosure; Page 14; 86pp; English.
XX
CC This sequence is the protein C GLA (gamma-carboxyglutamic acid)
CC domain. The invention relates to a vitamin K-dependent polypeptide
CC comprising a modified GLA domain containing an amino acid substitution
CC which enhances membrane binding of the modified polypeptide as compared
CC to the native polypeptide. The polypeptide is used to treat a clotting
CC disorder by decreasing or increasing clot formation. Modification of the
CC GLA domain results in a protein which has enhanced membrane binding
CC affinity as compared to the native protein.
XX
SQ Sequence 44 AA:

Query Match 88.0%; Score 176; DB 20; Length 44;
Best Local Similarity 97.7%; Pred. No. 2e-22;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ANSFLXLRHGSIXRCIXICDFXXAKXIFONVDDTLAFMSKH 44
Db 1 ansflxlrhgsixrcixicdfxxakxifgnvddtlafmskh 44
|||||

RESULT 2
ID AAB36402 standard; peptide; 44 AA.
XX
AC AAB36402:
XX
DT 27-FEB-2001 (first entry)
XX
DE Human protein C gamma-carboxyglutamic acid domain SEQ ID NO:1.
XX
KW Vitamin K-dependent protein; factor VII; protein C; GLA domain;
KW gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
KW factor X; prothrombin; enhanced membrane binding affinity;
KW clot formation; thrombolytic; haemostatic; bleeding disorder;
KW thrombosis; clotting disorder; haemophilia A; haemophilia B;
KW liver disease.
XX
OS Homo sapiens.
XX
PN MO20006753-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US11416.
XX
PR 29-APR-1999; 99US-0302239.
XX
PA (MINU) UNIV MINNESOTA.
XX
PI Neisestuen GL;
XX
DR WPI; 2001-007226/01.
XX
PT Novel vitamin K-dependent polypeptide useful for treating clotting
PT disorders such as thrombosis and hemophilia, comprises modified
PT gamma-carboxy glutamic acid domain that enhances membrane binding
PT affinity -
XX
PS Example 5; Page 42; 81pp; English.
XX
CC The present invention describes a vitamin K-dependent polypeptide (I)
CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having
CC at least one amino acid substitution, that enhances membrane binding
CC affinity and the activity of the polypeptide relative to a corresponding
CC native vitamin K-dependent polypeptide and inhibits clot formation.
CC (I) can have thrombolytic and haemostatic activities, and can be used
CC as an inhibitor of clot formation. (I) is useful for decreasing clot

CC formation in a mammal, a factor VII or factor IX containing a modified
CC GLA domain is useful for increasing clot formation and for treating a
CC bleeding disorder, including thrombosis and clotting disorders such as
CC haemophilia A, haemophilia B and liver disease. The present sequence
CC represents a human protein C GLA domain sequence, given in the
CC exemplification of the present invention.
XX
SQ Sequence 44 AA:

Query Match 88.0%; Score 176; DB 22; Length 44;
Best Local Similarity 97.7%; Pred. No. 2e-22;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ANSFLXLRHGSIXRCIXICDFXXAKXIFONVDDTLAFMSKH 44
Db 1 ansflxlrhgsixrcixicdfxxakxifgnvddtlafmskh 44
|||||

RESULT 3
ID AAW75710 standard; protein; 45 AA.
XX
AC AAW75710:
XX
DT 08-DEC-1998 (first entry)
XX
DE Partial human protein C amino acid sequence.
XX
KW Gamma carboxyglutamic acid; human protein C; GLA domain; chimera;
KW pRC/RSV; RSV-PC; amplification, PCR, primer; transfection; anticoagulant;
KW human 293 cell; Protein S; myocardial infarction; venous thrombosis;
KW disseminated intravascular coagulation; thromboembolic disease; lupus;
KW adult respiratory distress syndrome; factor V Leiden; stroke.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 6 /note= "Gamma carboxyglutamic acid"
FT Misc-difference 7 /note= "Gamma carboxyglutamic acid"
FT Misc-difference 14 /note= "Gamma carboxyglutamic acid"
FT Misc-difference 16 /note= "Gamma carboxyglutamic acid"
FT Misc-difference 19 /note= "Gamma carboxyglutamic acid"
FT Misc-difference 20 /note= "Gamma carboxyglutamic acid"
FT Misc-difference 25 /note= "Gamma carboxyglutamic acid"
FT Misc-difference 26 /note= "Gamma carboxyglutamic acid"
FT Misc-difference 29 /note= "Gamma carboxyglutamic acid"
FT Misc-difference 29 /note= "Gamma carboxyglutamic acid"
XX
PN WO9820118-A1.
XX
PD 14-MAY-1998.
XX
PE 07-NOV-1997; 97WO-US20376.
XX
PR 25-JUL-1997; 97US-0053768.
XX
PR 08-NOV-1996; 96US-0745254.
XX
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX
PI Esmon CT, Smirnov M;
XX
DR WPI; 1998-286934/25.
XX
PT Protein C chimeric proteins for use as anticoagulants - having gamma


```

xx      The PC polypeptides indicated in the Features Table inhibit
cc      coagulation if they prevent binding of serine protease to natural
cc      substrates), esp. when admin. to give an intravascular blood
cc      concn. of 0.1-100 (pref. 0.5-10) microm.
cc      NB: Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are described
cc      in the specification but have not yet been added to the SEQUENCE
cc      LISTING.
xx
xx      Sequence      419 AA;
sq

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RESULT	6
AAW72753	AAW72753 standard; protein; 419 AA.
AAW72753	
08-JAN-1999	(first entry)
Primary structure of activated human protein C.	
Human; activated protein C; primary structure; autodegradation; purification; processing; intravascular coagulation; thrombotic stroke; deep vein thrombosis; pulmonary embolism; peripheral arterial thrombosis; emboli; heart; peripheral artery; acute myocardial infarction; disseminated intravascular coagulation; acute precapillary occlusion; postcapillary occlusion; transplantation; retina thrombosis.	
Homo sapiens.	
Key	Location/Qualifiers
Disulfide-bond	17..22
Disulfide-bond	50..69
Disulfide-bond	80..89
Disulfide-bond	98..109
Disulfide-bond	105..118
Disulfide-bond	120..133
Disulfide-bond	141..277
Misc-difference	153
/note-	"unspecified"
Misc-difference	154
/note-	"unspecified"
Misc-difference	155
/note-	"unspecified"
Misc-difference	156
/note-	"unspecified"
Misc-difference	157
/note-	"unspecified"
Misc-difference	158
/note-	"unspecified"
Misc-difference	159
/note-	"unspecified"
Misc-difference	160
/note-	"unspecified"
Misc-difference	161
/note-	"unspecified"
Misc-difference	162
/note-	"unspecified"
Misc-difference	163
/note-	"unspecified"
Misc-difference	164
/note-	"unspecified"
Misc-difference	165
/note-	"unspecified"

FT	Misc-difference	166	/note= "unspecified"
FT	Misc-difference	167	/note= "unspecified"
FT	Misc-difference	167	/note= "unspecified"
FT	Misc-difference	168	/note= "unspecified"
FT	Misc-difference	169	/note= "unspecified"
FT	Disulfide-bond	196..212	/note= "unspecified"
FT	Disulfide-bond	331..345	
FT	Disulfide-bond	356..384	
XX			
PN	EP875563-A2.		
XX			
PD	04-NOV-1998.		
XX			
PF	28-APR-1998;	98EP-0303312.	
XX			
PR	28-APR-1997;	97US-0045255.	
XX			
PA	(ELIL) LILLY & CO ELI.		
XX			
PI	Baker JC, Carlson AD, Huang L, Sheliha TA;		
DR	WPI: 1998-559430/48.		
XX			
PT	Improved processing and purification of activated protein C -		
PT	comprises processing aqueous solution at specified ionic strength		
PT	and pH to reduce the amount of autodegradation products		
XX			
PS	Disclosure: Fig 1; 7pp; English.		
XX			
CC	An improved method has been developed of processing an aqueous solution		
CC	of activated protein C (apc). The method comprises conducting the		
CC	processing at an ionic strength greater than 150 mM and a pH of 5.5-6.3.		
CC	The present sequence represents the primary structure of activated human		
CC	protein C, used to assist in illustrating the autodegradation pathways		
CC	described in the present invention. The apc is used for treating a		
CC	variety of acquired disease states involving intravascular coagulation		
CC	e.g. thrombotic stroke, deep vein thrombosis, pulmonary embolism,		
CC	peripheral arterial thrombosis, emboli originating from the heart or		
CC	intravascular coagulation and acute pre- or postcapillary occlusions		
CC	including transplantations or retina thrombosis. The process minimises		
CC	the percentage of autodegradation products forming at most 10%,		
CC	preferably below 5% of des(1-9) apc and des(1-10) apc by weight, to		
CC	achieve a more potent, higher purity apc pharmaceutical preparation.		
XX			
XX			
SO	Sequence 419 AA;		
Query Match 88.0%; Score 176; DB 19; Length 419;			
Best Local Similarity 77.3%; Pred. No. 2.2e-21;			
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;			
OY	1 ANSFLXLRHGSIXKXCIXICDFXKXAKXIRQVNDTIAFMKSH 44		
DB	1 ansflxlrrhgsllrccleelcdfeekellgnvddtlaifwskh 44		
RESULT 7			
AAB36894			
XX	AAB36894 standard; Protein: 419 AA.		
AC	AAB36894;		
XX			
DT	26-FEB-2001 (first entry)		
XX			
DE	Human protein C derivative 1.		
XX			
XX	Protein C; human; vascular occlusive; burn; transplantation;		
XX	deep vein thrombosis; sickle cell; thalassemia;		

